

46875
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From: Jiang, Dong
Sent: Monday, July 16, 2001 4:11 PM
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Please search 1 to 322 of SEQ ID NO:2, and
1 to 320 of SEQ ID NO:4

-issued
-commercial

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Dong Jiang (78243)
703-305-1345
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Art Unit 1646

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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

STAFF USE ONLY

Searcher: PS Neenan - laly
 Searcher Phone #: 308-4501
 Searcher Location: Biotec lab
 Date Searcher Picked Up: 7/17/01
 Date Completed: 7/17/01
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Type of Search

NA Sequence (#) _____
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 Structure (#) _____
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us-09-488-728-4_copy_1_320.rspt

Page 1

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: July 17, 2001, 11:20:41 ; Search time 38.21 Seconds
(without alignments)
1108.024 Million cell updates/sec

Title: US-09-488-728-4_COPY_1_320
Perfect score: 1764
Sequence: 1 MGAARSPSAVPGPLIGLL.....VSCPEMPDTPPIPDYMLW 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_16:*
2: SP_Archaea:*
3: SP_Bacteria:*
4: SP_Fungi:*
5: SP_Human:*
6: SP_Invertebrate:*
7: SP_Mammal:*
8: SP_Misc:*
9: SP_Organelle:*
10: SP_Phage:*
11: SP_Plant:*
12: SP_Rodent:*
13: SP_Unclassified:*
14: SP_Vertebrate:*
15: SP_Virus:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1764	100.0	866	4	043844	043844 homo sapien
2	1254	71.1	426	4	060943	060943 mus musculu
3	286	16.2	426	4	02NRML4	02NRML4 homo sapien
4	284	16.1	502	4	02NRML6	02NRML6 mus musculu
5	272.5	15.4	499	11	03UIP3	03UIP3 mus musculu
6	220	12.5	288	4	02NRML5	02NRML5 mus musculu
7	166.5	9.4	218	11	02UIP2	02UIP2 mus musculu
8	97.5	5.5	398	5	061939	061939 caenorhabdi
9	96.5	5.5	800	5	09U980	09U980 drosophila
10	96.5	5.5	800	5	09U980	09U980 drosophila
11	93	5.3	1204	4	09U980	09U980 homo sapien
12	93	5.3	1209	4	09U980	09U980 homo sapien
13	92.5	5.2	509	11	09U980	09U980 drosophila
14	92	5.2	593	10	09U980	09U980 drosophila
15	92	5.2	623	10	09U980	09U980 drosophila
16	90.5	5.1	260	7	09U980	09U980 drosophila
17	90.5	5.1	744	5	09U980	09U980 drosophila
18	90.5	5.1	1870	14	09U980	09U980 fowlpox vir
19	90.5	5.1	1870	14	09U980	09U980 fowlpox vir

20	90	5.1	509	11	P97710	P97710 rattus norv
21	89.5	5.1	418	11	070426	070426 rattus norv
22	89.5	5.1	471	11	09RIE9	09RIE9 mus musculu
23	88.5	5.0	1144	10	040392	040392 nicotiana g
24	88	5.0	679	10	03ZMD7	03ZMD7 arabidopsis
25	88	5.0	4340	2	030764	030764 streptomyces
26	87.5	5.0	234	10	09SN88	09SN88 arabidopsis
27	87.5	5.0	337	11	035325	035325 mus musculu
28	87	4.9	1216	5	P91092	P91092 caenorhabdi
29	87	4.9	1341	5	062884	062884 rattus norv
30	87	4.9	1515	4	09NU48	09NU48 homo sapien
31	87	4.9	1522	4	09NU48	09NU48 homo sapien
32	86.5	4.9	249	14	09EB19	09EB19 human rotav
33	86.5	4.9	4578	13	042181	042181 fugu rubrip
34	86	4.9	397	11	035118	035118 mus musculu
35	85.5	4.8	323	11	09KXW9	09KXW9 streptomyces
36	84.5	4.8	397	11	055243	055243 mus musculu
37	84.5	4.8	1047	4	09HC39	09HC39 homo sapien
38	84.5	4.8	1047	4	09HB89	09HB89 homo sapien
39	84.5	4.8	1047	4	09HB89	09HB89 brachydanio
40	84.5	4.8	1059	13	09DE49	09DE49 schizosacch
41	84.5	4.8	1151	3	013987	013987 schizosacch
42	84.5	4.8	1442	4	092735	092735 homo sapien
43	84.5	4.8	1956	4	043154	043154 homo sapien
44	84	4.8	244	11	09ES44	09ES44 rattus norv
45	84	4.8	244	11	09ES44	09ES44 rattus norv

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	866 AA.
043844	043844	01-JUN-1998 (TREMBLrel. 06, Created)		
AC	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-JUN-1998 (TREMBLrel. 06, Last annotation update)			
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)			
DT	IL-17 RECEPTOR.			
DE	Homo sapiens (Human).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98035683; PubMed=9367539;			
RA	Yao Z., Spriggs M.K., Derry J.M.J., Strickline L., Park L.S.,			
RA	Vandenbos T., Zappone J., Painter S.L., Armitage R.J.;			
RT	"Molecular characterization of the human interleukin (IL)-17			
RT	receptor".			
RL	Cytokine 9:794-800(1997).			
DR	EMBL: U58917; AMB99730.1;			
SO	SEQUENCE 866 AA; 96121 MW; 88AF626A83F3FF70 CRC64;			

Query Match	Score	1764;	DB 4;	Length	866;
Best Local Similarity	100.0%;	Pred. No. 1.2e-164;			
Matches	320;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
1	MGAARSPSAVPGPLIGLL.....VSCPEMPDTPPIPDYMLW 320				
1	MGAARSPSAVPGPLIGLL.....VSCPEMPDTPPIPDYMLW 320				
61	SWIHPRNLTPSSPKDLOIOLHFAHTQGDLPVAHLEMTLOTDASTLYEGAEISVLOIN 120				
61	SWIHPRNLTPSSPKDLOIOLHFAHTQGDLPVAHLEMTLOTDASTLYEGAEISVLOIN 120				
121	TNERICVFEETSKLRHHRMRFTFSHFVYVDPDEEVYVHLPKPIPDGPNHOSKNF 180				
121	TNERICVFEETSKLRHHRMRFTFSHFVYVDPDEEVYVHLPKPIPDGPNHOSKNF 180				
181	LVPDEHARKVYTCMGSSGLMPDNITVETLEAHQLRVSTLANESTHQIILTSPPM 240				
181	LVPDEHARKVYTCMGSSGLMPDNITVETLEAHQLRVSTLANESTHQIILTSPPM 240				

Db 181 LVPDCEAHKMKVTPPCSSGSLMDPNITVETLEAHOLRVSEFTLMNSTHYQILITSPFHM 240
 QY 241 ENHSCFEHMHIPAPREEFHORSNVTLLRNKGGCRHOVOIOPEFSSCLMDCRHSAT 300
 Db 241 ENHSCFEHMHIPAPREEFHORSNVTLLRNKGGCRHOVOIOPEFSSCLMDCRHSAT 300
 QY 301 VSCPEMDPTPEPIPDYMLM 320
 Db 301 VSCPEMDPTPEPIPDYMLM 320

RESULT 2

Q60943 PRELIMINARY; PRT; 864 AA.
 AC Q60943;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DE INTERLEUKIN 17 RECEPTOR.
 GN IL17R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC TISSUE=THYMOMA ELD;
 RA MEDLINE=96111968; PubMed=8777726;
 RA Yao Z., Fanslow W.C., Seidlin M.F., Rousseau A.M., Painter S.L.,
 RA Comau M.R., Cohen J.I., Spriggs M.K.,
 RT "Hepesvirus Saltillo encodes a new cytokine, IL-17, which binds to a
 RT novel cytokine receptor."
 RL Immunity 3:811-821(1995).
 DR EMBL; U31993; AAC52357.1;
 DR MGI:107399; IL17L.
 SQ SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;

Query Match

Best Local Similarity 71.1%; Score 1254; DB 11; Length 864;
 Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

QY 1 MGAARSPSPVAPRLGILLGLVLAAPGASRLDHRALVCSOPGKNTYKNTCTD 60
 Db 1 MAIRRCMPVPEPRLGILLGLVLAAPGASRLDHRALVCSOPGKNTYKNTCTD 60
 QY 61 SMHPRNLTPSSPKDLOIOLAFHANTQOGLFPAHIEMLTQDASITYLEGAELSVQLN 120
 Db 61 SMHPRNLTPSSPKDLOIOLAFHANTQOGLFPAHIEMLTQDASITYLEGAELSVQLN 120
 QY 121 TNERLCVREFELSKLRHHRMRREFSHFVVDPODEXEVTVHNLPRIPGDPHOSKNF 180
 Db 121 TNERLCVREFELSKLRHHRMRREFSHFVVDPODEXEVTVHNLPRIPGDPHOSKNF 180
 QY 181 LVPDCEAHKMKVTPPCSSGSLMDPNITVETLEAHOLRVSEFTLMNSTHYQILITSPFHM 240
 Db 181 LVPDCEAHKMKVTPPCSSGSLMDPNITVETLEAHOLRVSEFTLMNSTHYQILITSPFHM 240
 QY 241 ENHSCFEHMHIPAPREEFHORSNVTLLRNKGGCRHOVOIOPEFSSCLMDCRHSAT 300
 Db 241 ENHSCFEHMHIPAPREEFHORSNVTLLRNKGGCRHOVOIOPEFSSCLMDCRHSAT 300
 QY 301 VSCPEMDPTPEPIPDYMLM 320
 Db 301 VSCPEMDPTPEPIPDYMLM 320

RESULT 3

Q60943 PRELIMINARY; PRT; 426 AA.
 AC Q60943;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DE IL-17B RECEPTOR.
 GN IL17BR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20317118; PubMed=10749887;
 RA Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,
 RA Ruben S.M., Wang W., Mathen K., Hodge V., Fisher C.L., Olsen H.,
 RA Carrell J.A., Ebner R.,
 RT "A novel cytokine receptor-11gand pair. Identification, molecular
 RT characterization, and in vivo immunomodulatory activity."
 RL J. Biol. Chem. 275:19167-19176(2000).
 DR EMBL; AF212365; AAF78776.1;
 KW Receptor.
 SQ SEQUENCE 426 AA; 47137 MW; D5B820CCFEC12E27 CRC64;

Query Match 16.2%; Score 286; DB 4; Length 426;
 Best Local Similarity 27.2%; Pred. No. 6,4e-20;
 Matches 83; Conservative 48; Mismatches 142; Indels 32; Gaps 8;

QY 16 LGLILLGLVLAAPGASRLDHRALVCSOPGKNTYKNTCTDSDSWHPRNLTPSSPKD 75
 Db 1 MSIVLSTLALC-----RSAYREFVQC--GSEFGSPPEMLDHDLPGLRD 47
 QY 76 LQIQLFHANTQOGLFPAHIEMLTQDASITYLEGAELSVL-OLNTNRLCYREF- 130
 Db 48 LVEPVTSVATGDSILMANSWLRADASTRLKATKICVTGKSNQSSVCRCNTTA 107
 QY 131 FLKLRHHRMRREFSHFVVDPODEXEVTVHNLPRIPGDPHOSKNFVDPDCEAHM 190
 Db 108 FQIQTRPSGKMTSYGFEVELNTYFICAHNIPANNKEDGPSKSNVFTSPGCLDHI 167
 QY 191 KVTTPCASSGSLMDPNITVETLEAHOLRVSEFTLMNSTHYQILITSPFHMENHSCFEHMH 250
 Db 168 KYKKCKVAKASLMDPNITACKNEIEVAVFTTPPGNRYMLI-----OHSILIFS 220
 QY 251 HIPAPREEFHORSNVTLLRNKGGCRHOVOIOPEFSSCLMDCRHSAT-VSCPEMDPT 309
 Db 221 QVEPHQKQOTASVTVPTGSEGA---TVQLEPYPCSDCIHRNGTVLDPQ---T 274
 QY 310 PEPIP 314
 Db 275 GVPFP 279

RESULT 4

Q60943 PRELIMINARY; PRT; 502 AA.
 AC Q60943;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DE IL-17 RECEPTOR HOMOLOG PRECURSOR.
 GN EVI27.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20273223; PubMed=10815801;
 RA Tian F., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
 RA Shaughnessy J.D. Jr.,
 RT "EVI27 encodes a novel membrane protein with homology to the IL17
 RL Oncogene 19:2098-2109(2000).
 DR EMBL; AF208110; AAF86051.1;-

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us-09-488-728-4_copy_1_320.rsp

KW Signal: Receptor. 13 POTENTIAL.
 FT SIGNAL 1 502 IL-17 RECEPTOR HOMOLOG
 CHAIN 14 9684A63EC123FF17 CRC64;
 SO SEQUENCE 502 AA: 53918 MW: 9684A63EC123FF17 CRC64;

Query Match 16.1%; Score 284; DB 4; Length 502;
 Best Local Similarity 26.9%; Pred. No. 1.2e-19;
 Matches 82; Conservative 49; Mismatches 142; Indels 32; Gaps 8;

DB 16 LGILLLLGVLPAGASIRLDRHALVCSQPGINCTVKNSTCILDSDWIPRNLTPSSPKD 47
 1 MSVLISIALALC-----RSAPRPTVOC--GSETGSPPMMLQHDLPEDLND 130
 QY 76 LQIQLHFAHTQGDLPVVAHIEWTLQTDASILYLEGALSVL-QLNTERLCVRFE- 107
 DB 48 LVEPVTSVATGDYSILMNVSILNRADASTIRLKATKICVYTKSNQSYSCVRCNTYA 190
 QY 131 FLKSLRHHRRMRFTFSHFVDDPEYEVYVHLLPKPIPDGPNHOSKNFLVPDCHEARM 167
 DB 108 FQOTRPSGKMTFSYIGPVELNTVYFIGAHNIPNANNEDGSMVSNTSPCLDHIM 250
 QY 191 KVTTPCMSSGLMDPNITVELEAHLRVSFILMNESTHYQILLTFPHMNHSCFEHM 220
 DB 168 KYKKCYKAGSLMDPNITACKKNEETVEVNTTPIGNRYMALI-----QHSIIIFS 309
 QY 251 HIRPREEFHORSNVTLLRLNKGCCRHQYOLOPFSSCLNDCLHSAT-VSCPEMPDT 309
 DB 221 QVPEHOKKORASVVIPTVGDSEGA---TVQLTPYFPICGSDICIRHKITVLCPO--T 274
 QY 310 PEPPI 314
 DB 275 GVPFP 279

RESULT 5
 Q9JIP3 PRELIMINARY; PRT: 499 AA.
 ID Q9JIP3
 AC 09JIP3; PRELIMINARY: PRT: 499 AA.
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE IL-17 RECEPTOR HOMOLOG PRECURSOR.
 GN EVI27.
 OS Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX 11
 RN SEQUENCE FROM N.A.
 RP MEDLINE-20273223; PubMed=10815801;
 RA Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
 RA Shaughnessy J.D. Jr.;
 RT "Evi27 encodes a novel membrane protein with homology to the IL17
 RT receptor";
 RL Oncogene 19:2098-2109(2000).
 DR EMBL: AF208108; AAF86049.1;
 KM SIGNAL 1 8
 FT CHAIN 9 499
 FT SEQUENCE 499 AA: 55617 MW: C66440430E3C31F3 CRC64;

Query Match 15.4%; Score 272.5; DB 11; Length 499;
 Best Local Similarity 27.6%; Pred. No. 1.6e-18; Indels 51; Gaps 11;
 Matches 89; Conservative 45; Mismatches 137;

QY 19 LILLGLVLPAGASIRLDRHALVCSQPGINCTVKNSTCILDSDWIPRNLTPSSPKD 78
 DB 1 MLVLLITIA-----RSAPRPTVOC--GSETGSPPMMLQHDLPEDLND 50
 QY 79 QLFHFAHTQGDLPVVAHIEWTLQTDASILYLEGALSVL-QLNTERLCVRFE---FLS 133
 DB 1 MLVLLITIA-----RSAPRPTVOC--GSETGSPPMMLQHDLPEDLND 50

DB 51 ELVTSVAEEFSLIMNISILRADASTIRLKATKICVSGKNMNSYSCVRCNTYEAQS 110
 QY 134 KLRRHRRMRFTFSHFVDDPEYEVYVHLLPKPIPDGPNHOSKNFLVPDCHEARM 193
 DB 111 QTRPSGKMTFSYIGPVELNTVYFIGAHNIPNANNEDGSMVSNTSPCLDHIM 170
 QY 194 TPCMSGSLMDPNITVELEAHLRVSFILMNESTHYQILLTFPHMNHSCFEHM 248
 DB 171 KQTEAGSLMDPNITACKKNEETVEVNTTPIGNRYMALI-----QHSIIIFS 230
 QY 249 MHIRPREEFHORSNVTLLRLNKGCCRHQYOLOPFSSCLNDCLHSAT-VSCPEMP 307
 DB 231 SVAPLPTSESE-----GAV--VQLTPYFPICGSDICIRHKITVLCPO--T 270
 QY 308 DTPEDIP-----DYMPLM 320
 DB 271 -TSAPIPDDNRMLGMLPLF 291

RESULT 6
 Q9NRM5 PRELIMINARY; PRT: 288 AA.
 ID Q9NRM5
 AC 09NRM5; PRELIMINARY: PRT: 288 AA.
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE TRUNCATED IL-17 RECEPTOR HOMOLOG PRECURSOR.
 GN EVI27.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 OX 11
 RN SEQUENCE FROM N.A.
 RP MEDLINE-20273223; PubMed=10815801;
 RA Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
 RA Shaughnessy J.D. Jr.;
 RT "Evi27 encodes a novel membrane protein with homology to the IL17
 RT receptor";
 RL Oncogene 19:2098-2109(2000).
 DR EMBL: AF208111; AAF86052.1;
 KM SIGNAL 1 13
 FT CHAIN 14 288
 FT SEQUENCE 288 AA: 31773 MW: CD8EB2C0C235FBB CRC64;

Query Match 12.5%; Score 220; DB 4; Length 288;
 Best Local Similarity 26.8%; Pred. No. 1.3e-13; Indels 18; Gaps 4;
 Matches 60; Conservative 37; Mismatches 109;

QY 16 LGILLLLGVLPAGASIRLDRHALVCSQPGINCTVKNSTCILDSDWIPRNLTPSSPKD 47
 DB 1 MSVLISIALALC-----RSAPRPTVOC--GSETGSPPMMLQHDLPEDLND 130
 QY 76 LQIQLHFAHTQGDLPVVAHIEWTLQTDASILYLEGALSVL-QLNTERLCVRFE- 107
 DB 48 LVEPVTSVATGDYSILMNVSILNRADASTIRLKATKICVYTKSNQSYSCVRCNTYA 190
 QY 131 FLKSLRHHRRMRFTFSHFVDDPEYEVYVHLLPKPIPDGPNHOSKNFLVPDCHEARM 167
 DB 108 FQOTRPSGKMTFSYIGPVELNTVYFIGAHNIPNANNEDGSMVSNTSPCLDHIM 250
 QY 191 KVTTPCMSSGLMDPNITVELEAHLRVSFILMNESTHYQILLTFPHMNHSCFEHM 220
 DB 168 KYKKCYKAGSLMDPNITACKKNEETVEVNTTPIGNRYMALI 211

RESULT 7
 Q9JIP2 PRELIMINARY; PRT: 218 AA.
 ID Q9JIP2
 AC 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
 GN IL-17 RECEPTOR HOMOLOG SHORT ISOFORM PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20273223; PubMed=10815801;
 RA Tian E., Sawyer J.R., Latgaspada D.A., Jenkins N.A., Copeland N.G.,
 RA Staughton J.D., Jr.;
 RT "Ev127 encodes a novel membrane protein with homology to the IL17
 receptor.";
 RL Oncogene 19:2098-2109(2000).
 DR EMBL: AF208109; AAF6050.1; -
 DR InterPro: IPR002259; -
 DR ProDom: PD005103; -; 1.
 KW Signal; Receptor.
 FT SIGNAL
 FT CHAIN
 SQ SEQUENCE 218 AA; 218 POTENTIAL. IL-17 RECEPTOR HOMOLOG SHORT ISOFORM.
 Best Local Similarity 28.28; Score 166.5; DB 11; Length 218;
 Matches 51; Conservative 32; Mismatches 83; Indels 15; Gaps 5;

Query Match
 Best Local Similarity 28.28; Score 166.5; DB 11; Length 218;
 Matches 51; Conservative 32; Mismatches 83; Indels 15; Gaps 5;
 QY 19 LLLILGLVLAGGASLRLDHRALVCSQPLNCTLVKNSCTLDLSWTHPRNLPSSPKDQI 78
 DB 1 MLVLVILIA-----ASC-----RSALPREPTIQ--GSETGSPSEWVQHLPGLDRLQV 50
 QY 79 QLFHANTQGGDLFPVAHIEWTLQTDASTILYEGAEISYL-OLANTNERLCVFE-----FLS 133
 DB 51 ELVKTQSVAAEEFSIIMILRADASTRLKATKICVSGKNNNSVCRCANTFAFOS 110
 QY 134 KLRHHRMRFFEFHFVVDPODEYVYVHLKRPIDGDPNHSKNLVDPCSHARKVT 193
 DB 111 QTRPGSGKWTFSYGFVELSTLYLSAHNIPNANNMEDSPSLSVNTSGCTRENTVEVT 170
 QY 194 T 194
 DB 171 S 171

RESULT 8
 ID 061939 PRELIMINARY; PRT; 398 AA.
 AC 061939;
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 GN T24A6.8 PROTEIN.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RX None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RP [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Taich A., Gattlung S., Le T.T.;
 RT "The sequence of C. elegans cosmid T24A6.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
 DR EMBL: AF068713; AAC17795.2; -
 DR HSP; P10828; 2N1L.
 DR InterPro: IPR000536; -
 DR InterPro: IPR001628; -
 DR Pfam: PF00104; hormone_rec; 2.
 DR Pfam: PF00105; zf-C4; 2.
 DR PRINTS: PR00047; STEROIDFINGER.
 DR SMART: SM00430; HOL1; 1.
 DR SMART: SM00399; ZnF_C4; 1.
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
 KW Zinc-finger.
 SQ SEQUENCE 398 AA; 46295 MW; DD051AE817F8A437 CRC64;

Query Match
 Best Local Similarity 20.58; Score 97.5; DB 5; Length 398;
 Matches 66; Conservative 38; Mismatches 89; Indels 129; Gaps 16;
 QY 39 RALVCSQP--GLNCYV-----KSTCLDLSWTHPRN----- 67
 DB 33 KCMVCAVRPHAGYHCDVATCKGCKTFRRMCLRGKICSTSGDCYDLKRNPSPLNCRPC 92
 QY 68 -----LTPSSPKDQI-----QLHFAHTQ--QGDLPVAHIEWTLQTDASTILY 108
 DB 93 RKRKOLLVGMNPKALIDGSMILSEKOVHNEODIOCTIDVLSLEAKTEQSKCAVNP 152
 QY 109 -----LEGAEISYLQMTNER-----LCVFEFESKLRH-----HIRRRRF 144
 DB 153 WTNIRLKLILSPKLSMDKSVGTFFPDWPLCPYEPDQIVHRDIQSSPFRKQWRFSNL 212
 QY 145 -----TSHR-----VVDPODEYVYVHLKRPD-----PDG----- 171
 DB 213 MTAVEYTKTFSFFHDLSPDQIHLKHVYIGLANFTYTYTLKKNFDLRLPDGTQRPV 272
 QY 172 -DPNH-----QSKNFLVPDCEHARKVTPPCSSGSLMDPNTVETLEAHLRVSFT 222
 DB 273 NEPHYCAHTVPPGPMKRIKIQNEFLILKILFVC-----NPAVPLNLSKH---AQFV 320
 QY 223 LWNSTHYQILLTSPHNHNS 244
 DB 321 IERKHHYSNILLKY-CLQNYNS 341

RESULT 9
 ID 090980 PRELIMINARY; PRT; 800 AA.
 AC 090980;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 GN CAP BINDING PROTEIN 80.
 GN CBP80 OR BG-94H4.3 OR CG7035.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OREGON R; TISSUE-IMAGINAL DISC;
 RA Lewis J.D.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A023870; CAB53186.1; -
 DR FlyBase; Fbn0022942; CBP80.
 SQ SEQUENCE 800 AA; 93070 MW; 7C9E7948ABD876B6 CRC64;

RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Strycharz R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-X., Massaman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
 "The genome sequence of *Drosophila melanogaster* ";
 Science 287:2185-2195(2000).
 RL [2]
 RN
 RP SEQUENCE OF 1-348 FROM N.A.
 RP
 RA Perraz C., Vidal S., Brun C., Bucheton A., Demaille J.G.:
 "Sequencing the distal X chromosome of *Drosophila melanogaster*."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-348 FROM N.A.
 RP
 RA Benos P.:
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AE003431; AAF45970.1; -
 DR EMBL: AL031766; CAA21136.1; -
 SR Flybase: FBgn0022942; Cpp80.
 SO SEQUENCE 800 AA; 93226 MW; 4D90C157E9A33B9B CRC64;

Best Local Similarity 22.3%; Pred. No. 1.8; Matches 88; Conservative 36; Mismatches 112; Indels 158; Gaps 23;

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OY 29 GGAALRLDRAALVCSOPGLNCTVKNSTCLDDSWIHRNLTPTS-----S 72
DB 704 GGHSHALL--RLATATPHL-----CIVDWICEEETGTGTDALLRMLLNNAKNHS 753
OY 73 PKDL-----OIQLFHAHTOQGDLPVAHLEMTLQOTASILYLEGALSVL 117
DB 754 PKLOAFASAVPVNHTQVQIIEHLILLASSELTPAEV---LTSMSQDLNSGVPRILL 810
OY 118 Q-----LNT--NERLCV-----RPEPLSKLRHHRRRFRFESHVVDP----- 153
DB 811 QVANKLMAVLTNTPMRRLMWTGNALOPSIKFY-----ROOKTQNDLMDPLIVLC 863
OY 154 DOEYEVTHLKPRIIPDGPBNHOSKNFLVPDCEH--ARKKVT---TPCMS-----GSLW 203
DB 864 DGR-----VHRCP-PLMD--ITLHMLNGYLASAKAYLSAHLKETEDRPSQNTTIGLVGOTD 917
OY 204 DPNITVEITLHAQLRVSFTLWNESTHYOILLTFSPHMENHSCFEHMHHPAPRPEEFHQR 263
DB 918 APEVTR-----ELKNALLAADSAAVOILL-----EICLPTEEKANG 956
OY 264 SNVTLTLRNL-----KG-----CCRHOVOIQPFSSCLNDCLRHSATVS-- 302
DB 957 VNPDSLRLNVOVSITTSAPNKGMEGEDNLCNREVO-----CLICCLLHOMYIADP 1009
OY 303 -----CPMDPTPEPIP-----DYMP 318
DB 1010 NIAKLVHFGYPCCLLPPLTVAGIPSMHICLDFIP 1043

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RESULT 12
Q9ULD3 PRELIMINARY; PRT; 1209 AA.
AC 09ULD3; 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DE 01-MAY-2000 (Tremblrel. 13, last annotation update)
GN KIA1287 PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K., Kikuno R., Hirose M., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT for large proteins in vitro.";
RL DNA Res. 6:337-345(1999).
DR EMBL; AB03113; BAA86601.1; -;
FT NON-TER
SQ SSOURCE 1209 AA; 134941 MW; BF44BD9971A37B9 CRC64;

Query Match
Best Local Similarity 22.3%; Score 93; DB 4; Length 1209;
Matches 88; Conservative 36; Mismatches 112; Indels 158; Gaps 23;

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OY 29 GGAALRLDRAALVCSOPGLNCTVKNSTCLDDSWIHRNLTPTS-----S 72
DB 709 GGHSHALL--RLATATPHL-----CIVDWICEEETGTGTDALLRMLLNNAKNHS 758
OY 73 PKDL-----OIQLFHAHTOQGDLPVAHLEMTLQOTASILYLEGALSVL 117
DB 759 PKLOAFASAVPVNHTQVQIIEHLILLASSELTPAEV---LTSMSQDLNSGVPRILL 815
OY 118 Q-----LNT--NERLCV-----RPEPLSKLRHHRRRFRFESHVVDP----- 153

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DB 816 QVANKLMAVLTNTPMRRLMWTGNALOPSIKFY-----ROOKTQNDLMDPLIVLC 868
OY 154 DOEYEVTHLKPRIIPDGPBNHOSKNFLVPDCEH--ARKKVT---TPCMS-----GSLW 203
DB 869 DGR-----VHRCP-PLMD--ITLHMLNGYLASAKAYLSAHLKETEDRPSQNTTIGLVGOTD 922
OY 204 DPNITVEITLHAQLRVSFTLWNESTHYOILLTFSPHMENHSCFEHMHHPAPRPEEFHQR 263
DB 923 APEVTR-----ELKNALLAADSAAVOILL-----EICLPTEEKANG 961
OY 264 SNVTLTLRNL-----KG-----CCRHOVOIQPFSSCLNDCLRHSATVS-- 302
DB 962 VNPDSLRLNVOVSITTSAPNKGMEGEDNLCNREVO-----CLICCLLHOMYIADP 1014
OY 303 -----CPMDPTPEPIP-----DYMP 318
DB 1015 NIAKLVHFGYPCCLLPPLTVAGIPSMHICLDFIP 1048

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RESULT 13
Q9VGY6 PRELIMINARY; PRT; 1233 AA.
AC 09VGY6; 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DE CG14682 PROTEIN.
GN CG14682.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA Sutton G.G., Worland J.R., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abhyant A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Giordex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwan C.,
RA Jaitani M., Kalush F., Kapran G.H., Ke Z., Kennison J.A., Kethum K.A.,
RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Munkulov G., Mitsuhashi N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazozo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Search completed: July 17, 2001, 11:20:43
Job time: 162 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 17, 2001, 11:21:04 ; Search time 16.71 Seconds
(without alignments)
656,000 Million cell updates/sec

Title: US-09-488-728-4_COPY_1_320
Perfect score: 1764
Sequence: 1 MGARSPPSAVPEPLIGLIL.....VSCPEMPDRPEPIPYMPLM 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91.5	5.2	184	1	Q9VH95 drosophila
2	88.5	5.0	249	1	P18570 rotavirus (
3	88.5	5.0	1402	1	P39806 drosophila
4	88	5.0	1210	1	P00533 homo sapien
5	87.5	5.0	1714	1	P28668 drosophila
6	86	4.9	439	1	P44398 haemophilus
7	86	4.9	603	1	P09172 homo sapien
8	85	4.8	607	1	P09898 schizosach
9	84.5	4.8	1058	1	P57678 homo sapien
10	83	4.7	191	1	P51526 anas platyr
11	83	4.7	275	1	P97760 mus musculu
12	83	4.7	740	1	P35852 lactobacill
13	81.5	4.6	416	1	P11279 homo sapien
14	81.5	4.6	558	1	O75144 homo sapien
15	81	4.6	275	1	P19387 homo sapien
16	81	4.6	397	1	P79778 gallus gall
17	81	4.6	808	1	Q02381 hepatitis a
18	80.5	4.6	1164	1	P52022 vldrio chol
19	80.5	4.6	1197	1	P30855 escherichia
20	79.5	4.5	4753	1	O04833 caenorhabdi
21	79	4.5	967	1	O9uqul1 rattus norv
22	78.5	4.5	1213	1	Q24325 drosophila
23	78	4.4	352	1	P00978 bos taurus
24	77.5	4.4	2242	1	O91437 mus musculu
25	77.5	4.4	337	1	P38484 homo sapien
26	77.5	4.4	410	1	P13473 homo sapien
27	77.5	4.4	587	1	P05932 homo sapien
28	77.5	4.4	1018	1	P10643 homo sapien
29	77.5	4.4	1018	1	P79987 gallus gall
30	77	4.4	155	1	P74739 synecocyst
31	77	4.4	459	1	P18711 homo sapien
32	77	4.4	484	1	O13289 candida alb

34	77	4.4	903	1	AGLU_SPIOL	O04893 spinacia ol
35	77	4.4	961	1	ACON_MYCAV	O08451 mycobacteri
36	77	4.4	1015	1	HIRA_MOUSE	O61666 mus musculu
37	77	4.4	1210	1	EGFR_MOUSE	O01279 mus musculu
38	77	4.4	1587	1	SUR2_CAEEL	O10669 caenorhabdi
39	76.5	4.3	432	1	BRAC_XENLA	P24781 xenopus lae
40	76.5	4.3	604	1	VGLE_SYVD	O04548 simian vari
41	76.5	4.3	2255	1	RRPL_SVS	O08434 simian viru
42	76.5	4.3	2255	1	RRPL_SYSWR	O03396 simian viru
43	76	4.3	484	1	CATP_CANTR	P07820 candida tro
44	76	4.3	644	1	YEN9_YEAST	P40032 saccharomyc
45	76	4.3	879	1	DPOL_MHVI	P03160 woodchuck h

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	184 AA.
YC17_DROME				
AC	09YH95:			
DT	01-OCT-2000 (Rel. 40, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	HYPOTHETICAL PROTEIN CG16817.			
GN	CG16817.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abilov R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Birkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,			
RA	Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,			
RA	Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,			
RA	Jajal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshnefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon R., Nusskern D.R., Paciel J.M.,			
RA	Palazzo D.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,			
RA	Spier E., Spradling A.C., Stapleton M., Venter E., Wang A.H., Wang X.,			
RA	Switskas R., Tecor C., Turner R., Venter E., Wang A.H., Wang X.,			
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Yao Q.A.,			
RA	Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,			
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,			
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;			
RT	"The genome sequence of Drosophila melanogaster."			
RL	Science 287:2185-2195(2000).			

Query Match 5.08; Score 88.5; DB 1: length 340

ZN_FING	432	454
ZN_FING	460	482

FT ZN.FING 845 867 C2H2-TYPE.
 FT ZN.FING 873 895 C2H2-TYPE.
 FT ZN.FING 905 927 C2H2-TYPE.
 FT ZN.FING 1336 1358 C2H2-TYPE.
 FT ZN.FING 1364 1386 C2H2-TYPE.
 FT SEQUENCE 1402 AA; 153745 MW; 4CDB2EE384F70AE5 CRC64;

Query Match 5.0%; Score 88.5; DB 1; Length 1402;
 Best Local Similarity 21.1%; Pred. No. 9; Mismatches 114; Indels 129; Gaps 18;
 Matches 74; Conservative 33;

1 MGABSPGAVGCPRLGL-----LILLGLVLPAGASTRLIDHALLVCQPGCLCTYKN 54
 542 MSFRASP--AFPG-LPGITRPPEMLLSGATAGTAGL---PPEFPQMGGLGALKH 594
 55 STCIDDSWHPNLT-----PSPKDIQIOLHFAHQGDLPVANIEMTLQTDASTYLE 110
 595 TH--DOSQDMPDLRKSSGSPSPHEEDNIAALPYKSELMEKEKEHTMEATR-----E 648
 111 GAEISVQLMTNERLCVFEFLSKLRHHRMRFTSHFYVDQEX-----EVTV 161
 649 SAEMEPPL-----EVRIKEER-----IDEDQMLQEGMOKPEPIA 685
 162 HHLKRP-----IPDGPNHQSKNPLVPCCEHARMKVTPCKSSGSLMDPNITVETLEAHOL 720
 686 YATPHPOCLIPTHAAKSPRSPLQC-HARL-----SLW-----720
 218 RVSTFLMESTHYOILTFSPHMENSCF-----EHMHITPAP-----RPEEFHQ 262
 721 -----CSHPTTSNHACAVLVGSGOTHLDOPLPTDNPVPTMPQEDFFAE 763
 263 RSNVTLT-----LRNLKGGCRHQVOIOFPFSSCLNDCLRHSATVSCP 304
 764 RPLPLFTSKTDHSDPISRPAGAHAIHRSPPFN-----IKHEMAAFVP 808

RESULT 4
 EGFR_HUMAN STANDARD; PRT; 1210 AA.

AC EGFR_HUMAN P00533; P06268; Q14225;
 ID 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112).
 GN EGFR OR ERBB1.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE-84219729; PubMed-6328312;
 RA Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
 RA Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
 RA Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.,
 RA "Human epidermal growth factor receptor cDNA sequence and aberrant
 RT expression of the amplified gene in A431 epidermoid carcinoma cells.",
 RT Nature 309:418-425(1984).
 [2]
 RP SEQUENCE OF 713-924 FROM N.A.
 RP MEDLINE-84196372; PubMed-6326261;
 RA Lin C.R., Chen W.S., Krueger W., Stolarsky L.S., Weber W.,
 RA Evans R.M., Verma I.M., Gill G.N., Rosenfield M.G.,
 RA "Expression cloning of human EGF receptor complementary DNA: gene
 RT amplification and three related messenger RNA products in A431
 RT cells.",
 RT Science 224:843-848(1984).
 [3]
 RP SEQUENCE OF 150-962 FROM N.A.
 RP MEDLINE-84245835; PubMed-6330563;
 RA Xu Y., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K., Ma D.P.,
 RA Roe B.A., Merlino G.T., Pastan I.,

RT "Human epidermal growth factor receptor cDNA is homologous to a
 RT variety of RNAs overproduced in A431 carcinoma cells.",
 RT Nature 309:806-810(1984).
 [4]
 RP SEQUENCE OF 1028-1210 FROM N.A.
 RP MEDLINE-85046483; PubMed-6093780;
 RA Stamen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G.,
 RA O'Malley B.W.,
 RA "Isolation of an evolutionarily conserved epidermal growth factor
 RT receptor cDNA from human A431 carcinoma cells.",
 RT Biochem. Biophys. Res. Commun. 124:125-132(1984).
 [5]
 RP SEQUENCE OF 1-29 FROM N.A.
 RP MEDLINE-88217333; PubMed-3329716;
 RA Haley J., Whittle N., Bennett P., Kinchington D., Ullrich A.,
 RA Waterfield M.,
 RA "The human EGF receptor gene: structure of the 110 kb locus and
 RT identification of sequences regulating its transcription.",
 RT Oncogene Res. 1:375-396(1987).
 [6]
 RP SEQUENCE OF 1-29 FROM N.A.
 RP MEDLINE-91107677; PubMed-1988448;
 RA Haley J.D., Waterfield M.D.,
 RA "Contributory effects of de novo transcription and premature
 RT transcript termination in the regulation of human epidermal growth
 RT factor receptor proto-oncogene RNA synthesis.",
 RT J. Biol. Chem. 266:1746-1753(1991).
 [7]
 RP SEQUENCE OF 1-29 FROM N.A.
 RP MEDLINE-85270438; PubMed-2991899;
 RA Ishii S., Xu Y.H., Stratton R.H., the promoter region of the human
 RA "Characterization and sequence of the promoter region of the human
 RT epidermal growth factor receptor gene.",
 RT Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985).
 [8]
 RP SEQUENCE OF 540.
 RA Kohda D.,
 RA Submitted (SEP-1997) to the SWISS-PROT data bank.
 [9]
 RP RECEPTOR ACTIVITY.
 RP MEDLINE-84191554; PubMed-6325948;
 RA Mroczkowski B., Mosig G., Cohen S.,
 RA "ATP-stimulated interaction between epidermal growth factor receptor
 RT and supercoiled DNA.",
 RT Nature 309:270-273(1984).
 [10]
 RP PHOSPHORYLATION.
 RP MEDLINE-88278137; PubMed-2543678;
 RA Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M.,
 RA Howk R., Givol D., Ullrich A., Schlessinger J.,
 RA "All autophosphorylation sites of epidermal growth factor (EGF)
 RT receptor and HER2/neu are located in their carboxyl-terminal tails.
 RT Identification of a novel site in EGF receptor.",
 RT J. Biol. Chem. 264:10667-10671(1989).
 [11]
 RP REVIEW.
 RP MEDLINE-87297456; PubMed-3039909;
 RA Carpenter G.,
 RA "Receptors for epidermal growth factor and other polypeptide
 RT mitogens.",
 RT Annu. Rev. Biochem. 56:881-914(1987).
 [12]
 RP FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
 RP AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
 RP VACCINIA VIRUS GROWTH FACTOR.
 RP CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP +
 RP PROTEIN TYROSINE PHOSPHATE.
 RP SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 RP -1- MISCELLANEOUS: BINDING OF EGF TO THE RECEPTOR LEADS TO
 RP INTERNALIZATION OF THE EGF-RECEPTOR COMPLEX, INDUCTION OF THE
 RP TYROSINE KINASE ACTIVITY, STIMULATION OF CELL DNA SYNTHESIS, AND
 RP CELL PROLIFERATION.
 RP -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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CC or send an email to license@isb.ch).

DR EMBL: X00588; CAA25240.1; -
DR EMBL: X06370; CAA29668.1; -
DR EMBL: X00663; CAA25282.1; -
DR EMBL: M38425; AAA63171.1; -
DR EMBL: M11234; AAA52370.1; -
DR PIR: A00641; GOHUE; -
DR PIR: A00642; GOHUE; -
DR HSP: P11362; IFGI; -
DR SWISS-2DPAGE; P00533; HUMAN.
DR MIM: 131550; -
DR InterPro: IPR000494; -
DR InterPro: IPR000719; -
DR InterPro: IPR001245; -
DR InterPro: IPR002174; -
DR Pfam: PF00757; Furin-like; 1.
DR Pfam: PF01030; Recep_L-domain; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transmembrane: Glycoprotein; Duplication; Receptor; Signal;
KW Translasease; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
FT CHAIN 1 24
FT TRANSEM 25 1210
FT DOMAIN 646 668
FT REPEAT 669 1210
FT REPEAT 390 600
FT DOMAIN 1025 1071
FT NP_BIND 712 979
FT BINDING 716 726
FT ACT_SITE 745 745
FT MOD_RES 837 837
FT MOD_RES 678 678
FT MOD_RES 1092 1092
FT MOD_RES 1110 1110
FT MOD_RES 1172 1172
FT MOD_RES 1197 1197
FT CARBOHYD 128 128
FT CARBOHYD 175 175
FT CARBOHYD 196 196
FT CARBOHYD 352 352
FT CARBOHYD 361 361
FT CARBOHYD 413 413
FT CARBOHYD 444 444
FT CARBOHYD 528 528
FT CARBOHYD 568 568
FT CARBOHYD 603 603
FT CARBOHYD 623 623
FT CONFLICT 540 540
SQ SEQUENCE 1210 AA: 134277 MW: DBA2A50BAEF6E0D CRC64;

Query Match 5 0%; Score 88; DB 1; Length 1210;
Best Local Similarity 22.6%; Pred. No. 8.3;
Matches 93; Conservative 45; Mismatches 156; Indels 118; Gaps 22;

QY 15 LIGILL-----LIGVAPGASURL-DHRALVCSOPGLNCTV---KNSTCDD-SWH- 64
Db 777 LIGVAPGASURL-DHRALVCSOPGLNCTV---KNSTCDD-SWH- 64
QY 65 ---PRNLTPSSPDLDIO-----LHFAHOGGD 89

Db 837 DLAAANLVKTPQHVKITDPGLAKLGAEEKEYHAGGRVPIKMALESILHRTYHOSD 896
QY 90 LEPVAVHIEWLQDASILY--LEGAEISVQLNTNERT-----CYRFEEL-----S 133
Db 897 VMSYGVTVWELMFSGKPYDGPASEISIS-LKESGRLPQPICTIIVYMIVKCMIDA 955
QY 134 KLNHHRNRWRFTHFVVPDDEYEVY---HLPKPI-----PDGPNHOSK 178
Db 956 DSRKPRRELIFESKARDP-GRVLYIGDERMHLPSPTDSNFYALDEEDMDVDYAD 1014
QY 179 NFLVDPCEHARKVY--TPCWSGSLMDPNITVETLEAQLRV-----SF----- 221
Db 1015 EYLIPQGFSSPSTSRPLLSISATSNSSTVACIDRNGLOSPKEDSFLOYSDDPT 1074
QY 222 -TLNVESTHYOILLT-----SFPMENHSCFEMNH-----IPARPEEFHOSNVTLT 270
Db 1075 GALTEDSIDDTFLPPEVYINOSVPRKRGVQNPVYHNOPLNAPSRDHYODPHSTAV- 1133
QY 271 RNKGGCCRHQVQIDPFSSCLN---DCLRHSAVSCPEMP-DTPEPIPDYMP 318
Db 1134 ---GNPEYLVNTVOP---TCVNSTFSDPAHMAOKGSHQSLNDNDYQODFFP 1178

RESULT 5
STEP-DROME STANDARD; PRT: 1714 AA.
AC P28668; Q9VCF5;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INITIATES: GLUTAMYL-TRNA
DE SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA
GN AATS-GLUPRO OR CG5394.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Nematoda; Drosophilidae; Drosophila.
NCBI_Taxid:7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92097547; PubMed=1756734;
RA Cerini C., Kerjan P., Astier M.,
RT "A component of the multisynthetase complex is a multifunctional
RL aminoacyl-trna synthetase";
RL EMBO J. 10:4267-4277(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=OREGON-R;
RA MEDLINE=97217441; PubMed=9063462;
RA Cerini C., Semeriva M., Gratecos D.,
RT "Evolution of the aminoacyl-trna synthetase family and the
RT organization of the Drosophila glutamyl-prolyl-trna synthetase gene.
RT mRNAs, exon structure of the gene, control of expression of the two
RL Eur. J. Biochem. 244:176-185(1997).
RP [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Pfeiffer B.D.,
RA Abell J.R., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotshakov S.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Harris A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbewam C.,
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Jallali M., Kalush F., Kraft C., Kravitz S., Kulp D., Lai X.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Pollard J., Puri V., Reese M.G.,
 RA Palazzo M., Plitman G.S., Pan S., Polard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Venter E., Wang A.H., Wang X.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster";
 RA Science 287:2185-2195(2000).
 RL Science 287:2185-2195(2000).
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
 CC -1- CATALYTIC ACTIVITY: ATP + L-PROLINE + TRNA(PRO) = AMP +
 CC -1- CATALYTIC ACTIVITY: ATP + L-PROLYL-TRNA(PRO).
 CC -1- PYROPHOSPHATE + L-PROLYL-TRNA(PRO).
 CC -1- SUBUNIT: COMPONENT OF THE MULTISYNTHETASE COMPLEX WHICH IS
 CC MONOSPECIFIC OF A BIFUNCTIONAL GLUTAMYL-PROLYL-TRNA SYNTHETASE, THE
 CC ARGINYL, P18, P48 AND P43.
 CC PROTEINS, AND ASPARTYL-TRNA SYNTHETASES AS WELL AS THREE AUXILIARY
 CC SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CLASS-I
 CC AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CLASS-II
 CC AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -1- SIMILARITY: CONTRAINS 6 "WHEP-TRS" DOMAINS.
 CC -----
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 CC -----
 CC EMBL: M7A104; AAA28594.1; -
 CC EMBL: U59923; AAC47469.1; -
 CC EMBL: AE003745; AAF56211.1; -
 CC PIR: S18644; S18644.
 DR HSP: P00962; 10RU.
 DR FLYbase: FBgn0005674; Aats-glu-pro.
 DR InterPro: IPR000738; -
 DR InterPro: IPR000924; -
 DR InterPro: IPR001412; -
 DR InterPro: IPR002106; -
 DR InterPro: IPR002314; -
 DR InterPro: IPR002316; -
 DR Pfam: PF00458; WHEP-TRS; 6.
 DR Pfam: PF00749; tRNA-synt.1c; 1.
 DR Pfam: PF00587; tRNA-synt.2b; 1.
 DR PRINTS: PRO0987; TRNASYNTHPRO.
 DR PRINTS: PRO1046; TRNASYNTHPRO.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
 DR PROSITE: PS00179; AA_TRNA_LIGASE_II_1; FALSE_NEG.
 DR PROSITE: PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
 DR PROSITE: PS00762; WHEP-TRS; 6.
 DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KM Multifunctional enzyme; Repeat.
 FT DOMAIN 170 754
 FT DOMAIN 755 800
 FT WHEP-TRS 1.

FT DOMAIN 827 872 WHEP-TRS 2.
 FT DOMAIN 901 946 WHEP-TRS 3.
 FT DOMAIN 980 1025 WHEP-TRS 4.
 FT DOMAIN 1055 1100 WHEP-TRS 5.
 FT DOMAIN 1129 1173 WHEP-TRS 6.
 FT DOMAIN 1174 1180 POLY-GLY.
 FT DOMAIN 1207 1716 PROLYL-TRNA SYNTHETASE.
 FT SITE 209 220 "HIGH" REGION.
 FT SITE 438 442 "KMSKS" REGION.
 FT BINDING 441 441 ATP (BY SIMILARITY).
 FT BINDING 102 106 TSPLE -> AF (IN REF. 3).
 FT CONFLICT 233 234 VC -> AF (IN REF. 3).
 FT CONFLICT 341 345 NTAQA -> KYVR (IN REF. 3).
 FT CONFLICT 583 583 K -> R (IN REF. 3).
 FT CONFLICT 692 692 L -> A (IN REF. 3).
 FT CONFLICT 753 753 T -> S (IN REF. 3).
 FT CONFLICT 802 802 P -> T (IN REF. 3).
 FT CONFLICT 873 873 P -> V (IN REF. 3).
 FT CONFLICT 887 887 G -> V (IN REF. 3).
 FT CONFLICT 1201 1201 P -> PA (IN REF. 3).
 FT CONFLICT 1461 1461 MISSING (IN REF. 3).
 FT CONFLICT 1587 1587 G -> V (IN REF. 3).
 SQ SEQUENCE 1714 AA; 189197 MW; 6FE8C58045E48A8C CRC64;
 Query Match 5.0%; Score 87.5; DB 1; Length 1714;
 Best Local Similarity 19.2%; Pred. No. 14; Mismatches 119; Indels 131; Gaps 17;
 Matches 71; Conservative 48;
 QY 32 SLRLDHRALVCSQPGINCTVKNSTCIDDSWIRPRLTSSP-----KDLQIQ--79
 DB 39 SLQPPDNLLVCH-----SNDVYL-----RALAPAPKYLXGFALEKRTQIDHW 83
 QY 80 LMFATQGGDLFPVAHITWLTQDAS-----ILVLEGAISVLOINTNERLCVFEEFLSK 134
 DB 84 LFSFSLCEBD-----LSMALSFLTSPLPVLYLVANKLTADPALENEHNSRFEFLAK 137
 QY 135 -LRHHRRMRFFSHFVYVDDPEETVYVHLPK-----PIPDGPNHOK 178
 DB 138 GIGOHQGR-----VDLTADPLQIKVLOSLEDKAKYKRSPOSSKECPATGKERKQEG 192
 QY 179 NLTVPDCEHAKMYTPPCSSGSLW-----DPNITVETL 212
 DB 193 FVLDLPGAEKMYVRRPPRASGLHGHAKAALLNOYALVCGTLINRFPDTPNPAKFTV 252
 QY 213 E-----AHOLRVSTFTMNSTHQLITSPHNEHSCF-----EHMHITAPRPE-- 258
 DB 253 EFENVILGDLQQLKEDVFTHTSNYFDMLDY-----CYRLIKSKAYVDDDPPEQM 305
 QY 259 --EFHOR-----SNVTLTLNIMG-----CCHQVQIQIPFSSGICNCLIRHS 298
 DB 306 KLERQVRASNRNSVYKNTLMEEWVKSGEKGONTACAKIDM-----SSPNCGRDP 360
 QY 299 ATVSCPEMP 307
 DB 361 TYRCKNEP 369
 RESULT 6
 ID XYLA_HAEIN STANDARD; PRT; 439 AA.
 AC P44398;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE XYLOSE ISOMERASE (EC 5.3.1.5).
 GN XYLA OR H11112
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 CC Haemophilus.
 CC NCBI_Taxid=727;
 RN [1]
 RP SEQUENCE FROM N.A.

CC STRAIN-RD / KW20 / ATCC 51907;
 RX MEDLINE-95350630; PubMed-7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerkela A.R., Saito G., Fitch W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shriver R., Liu L.-I., Glodok A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Sander D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Venier J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd.";
 RL Science 269:496-512(1995).
 CC -1- CATALYTIC ACTIVITY: D-Xylose = D-Xylofuranose.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
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 CC EMBL: U32791; AAC22766.1;
 DR HSSP: P45687; IAOE.
 DR TIGR: H1112;
 DR InterPro: IPR001998;
 DR Pfam: PF00259; Xylose_isom_1.
 DR PRINTS: PR00688; XYLOSEISOMERASE.
 DR PROSITE: PS00172; XYLOSE_ISOMERASE.1; 1.
 DR PROSITE: PS00173; XYLOSE_ISOMERASE.2; 1.
 KW Isomerase; Pentose shunt; Xylose metabolism; Magnesium.
 FT ACET SITE 101 101
 FT METAL 232 232
 FT METAL 268 268
 FT METAL 296 296
 FT METAL 339 339
 SO SEQUENCE 439 AA; 49896 MW; 24CD3CE4736A3E6A CRC64;

Query Match 4.9%; Score 86; DB 1; Length 439;
 Best Local Similarity 20.6%; Pred. No. 3.6; Mismatches 71; Indels 76; Gaps 10;
 Matches 47; Conservative 34;

DB 76 LQIOLHFAHT---OQGDPRVAHIEWTLOTASILEGALSVLQLTNRLCYRPEFL 132
 42 LRLAVCYWHTFCWNGNDPGLGSLERSWOKNSNL--LAGAE-----OKADIAEFL 90
 DB 133 SKLRHHRRMRTFSHFVVDPP---QEYEVTVHLLPRIDGPNQSKNFTLPDCEHA 188
 91 NKLGPY---YCFHDVDAIEPNSVREYVGNFH-----IYDLIERK 129
 DB 189 RMKY---TTPCMSSGSLMDPNVYETLEAHL-----RVSEFLAN 225
 130 QETGVKILMTANCFNPRMSCAATNPPEYFAMATQVFANAMATQRLGGENVLMG 189
 DB 226 ESTYQILISFPMENHS-----CFEHHMHP-----APREE 259
 190 GREYELMTIDKREKREQIGRPMQVVEHKKIKGKGLLIEPKOE 237

DE DOPAMINE BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-
 DE HYDROXYLASE) (DBH).
 GN DBH.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_Taxid-9606;
 RX SEQUENCE FROM N.A.
 RA MEDLINE-89160241; PubMed-2922261;
 RT Kobayashi K., Kurosawa Y., Fukita K., Nagatsu T.;
 RT "Human dopamine beta-hydroxylase gene: two mRNA types having
 RT different 3'-terminal regions are produced through alternative
 RT polyadenylation.";
 RL Nucleic Acids Res. 17:1089-1102(1989).
 RN [2]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE-88166633; PubMed-3443096;
 RA Lamouroux A., Vigny A., Faucon Biguet N., Darmon M.C., Franck R.,
 RA Henry J.-P., Mallet J.;
 RT "The primary structure of human dopamine-beta-hydroxylase: insights
 RT into the relationship between the soluble and the membrane-bound
 RT forms of the enzyme.";
 RL EMBL J. 6:3931-3937(1987).
 CC -1- FUNCTION: CONVERSION OF DOPAMINE TO NORADRENALINE.
 CC -1- CATALYTIC ACTIVITY: 3,4-DIHYDROXYPHENETHYLAMINE + ASCORBATE + O(2)
 CC = NORADRENALINE + DEHYDROASCORBATE + H(2)O.
 CC -1- COFACTOR: PQQ, COPPER, AND ASCORBATE.
 CC -1- PATHWAY: CATECHOLAMINE BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: EXISTS BOTH IN A SOLUBLE FORM (IN CHROMAFFIN
 CC ANCHORED BY AN UNCEAIVED SIGNAL PEPTIDE).
 CC -1- INDUCTION: ACTIVITY IS ENHANCED BY NERVE GROWTH FACTOR (IN
 CC SUPERIOR CERVICAL GANGLIA & ADRENAL MEDULLA). TRANS-SYNAPTIC
 CC STIMULATION WITH RESERPINE, ACETYLCHOLINE AND GLUCOCORTICOID.
 CC WHICH DIFFER IN ONE POSITION.
 CC -1- SIMILARITY: BELONGS TO THE COPPER TYPE II, ASCORBATE-DEPENDENT
 CC MONOOXYGENASE FAMILY.
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 CC EMBL: X13255; CA31631.1;
 DR EMBL: X13256; CA31632.1;
 DR EMBL: Y00096; CAA8285.1;
 DR PIR: S03020; S03020.
 DR PIR: S06283; S06283.
 DR MIM: 223360;
 DR InterPro: IPR000323;
 DR Pfam: PF01082; Cu2_monooxygen_1.
 DR PRINTS: PR00767; DEMONOXGNASE.
 DR PROSITE: PS00084; CU2_MONOOXYGENASE.1; 1.
 DR PROSITE: PS00085; CU2_MONOOXYGENASE.2; 1.
 KW Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Copper;
 KW Vitamin C; PQQ; Glycoprotein; Membrane; Signal; Polymorphism.
 FT CHAIN 26 603
 FT ACT SITE 216 216
 FT ACT SITE 398 398
 FT BINDING 398 398
 FT CARBOHYD 50 50
 FT CARBOHYD 170 170
 FT CARBOHYD 330 330
 FT CARBOHYD 552 552
 FT VARIANT 304 304
 A -> S (IN DBH-B).

FT CONFLICT 197 197 /FTID-VAR_002196.
 FT CONFLICT 535 535 R -> T (IN REF. 2).
 FT SEQUENCE 603 AA: 67627 MW: 39A7A897511DB5F CRC64;

Query Match 4.9%; Score 86; DB 1; Length 603;
 Best Local Similarity 19.4%; Pred. No. 5.3;
 Matches 54; Conservative

68 LPPSPKDLQIQLEAFHQGDLFPVAHIEWTL-----OTDASILY----- 108
 23 LGSASREPLRPHIPLDEGSL-----ELSNVSTOEAHQHQLLVRLKAGVLEMSDR 78
 109 --LEGALSTQLTNTERLCVREFLSKLRRHRRRTFTSHFVVDPODEY-VVHHNP 165
 79 GELENDLVVLTMD-----GDTAYPADMSDOKGTHIDPDDYQLLOVQRTP 126
 166 -----KPIPDGDPNHSKNFLVPDCEHAKKVTTPCKSSGSLMDPNITVETLEAHOL 217
 127 EGIULFLKREFGCDP-----KDYLIED-----GVHLVYGLIEPFRSLAINGSL 174
 218 RVSTLNNESHVQIILTSFPHM--NHSCEHMHHPARPEEFHORSNVTLTNTL-K 274
 175 QMGH-----GRVQLKPNIPERPELPDAD--TMEVQADNIQIPSOETTYWCYIKELPK 225
 275 GCCRHQ-VQIQPFSSCLNDLRHSATVSC-PEMPDTP 310
 226 GFSRHIIITKEPIVTKGNEALVHMEVFQCAPEMDSVP 263

RESULT 8

KAIB_SCHPO STANDARD; PRT: 607 AA.
 ID KAIB_SCHPO
 AC 009898;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE PROBABLE SERINE/THREONINE-PROTEIN KINASE C24B1.11C (EC 2.7.1.1-).
 GN SPAC24B1.11C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 NC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Odeh C., Churher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
 PROTEIN KINASES. HIGHLY SIMILAR TO YEAST DBP20 AND DBP2.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: 267757; CAAG1776.1;
 CC HSSP: P05132; ICP.
 DR InterPro: IPR000719;
 DR InterPro: IPR000961;
 DR InterPro: IPR002290;
 DR Pfam: PF00069; pkinase_1.
 DR Pfam: PF00433; pkinase_C_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
 DR Hypothetical protein; Transferase; Serine/threonine-protein kinase;
 KW ATP-binding; Phosphorylation.

FT DOMAIN 208 508 PROTEIN KINASE.
 FT NP_BIND 214 222 ATP (BY SIMILARITY).
 FT BINDING 237 237 ATP (BY SIMILARITY).
 FT ACT_SITE 331 331 BY SIMILARITY.
 FT MOD_RES 219 219 PHOSPHORYLATION (BY SIMILARITY).
 FT SEQUENCE 607 AA: 70491 MW: D92E5263C7341F1D CRC64;

Query Match 4.8%; Score 85; DB 1; Length 607;
 Best Local Similarity 21.7%; Pred. No. 6.5;
 Matches 60; Conservative

89 DLPFAHIEWTLQ-----TDAIYL-----EGALSVQLNTERLCVREFLSKLRRH 138
 258 DILTANSEMLVRLLYAFODTSNYIAMEFVPGDERTLISN-----GYLRDH 306
 139 HRRNRFTFSHVVDPDDEYVYHHLKPIPDGDPNHSKNFLVPDCEHAKKVTTPCKSS 198
 307 HAKYATEMLAID-----ALHOLGYIHRDLKP-----ENFVVGASGH--IKLTPGLS 353
 199 SGSLMDP-----NITVETLEAHOLRVSF-TL----- 223
 354 SGIKKKIESKIRLQGVNNVVPERSMREROVFTLLSDPYVAHSVGYSPDYMAPE 413
 224 -----WNESTHYQL-----LTSFP-----HMEN-HSCFEHMHHPARP 257
 414 VLKGVNHSVDYWSGCLMTBCLSGFPFGSSNVNETWSMLKWKRCFORPHY-DDPRD 472
 258 EEPHORSNV-----TLTLNLKGCCHROVOIQPFSS 288
 473 LEFNMDAMDFFCHCITDPKRFCSLQVMOHPYFS 509

RESULT 9

GEM4_HUMAN STANDARD; PRT: 1058 AA.
 ID GEM4_HUMAN
 AC P57678;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE COMPONENT OF GEMS 4 (GEMIN4) (P97).
 GN GEMIN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MASS SPECTROMETRY.
 RC MEDLINE=20191885; PubMed=10725331;
 RA Charroux B., Pellizzoni L., Parkinson R.A., Yong J., Shevchenko A.,
 RA Mann M., Dreyfuss G.;
 RT "Gemin4: a novel component of the SMN complex that is found in both
 RT gems and nucleoli.";
 RL J. Cell Biol. 148:1177-1186(2000).
 CC -1- FUNCTION: THE SMN COMPLEX PLAYS AN ESSENTIAL ROLE IN SPliceosomal
 CC SPLICING IN THE CYTOPLASM, AND IS REQUIRED FOR PRE-MRNA
 CC SPLICING IN THE NUCLEUS. GEMIN4 COULD SERVE AS A COFACTOR OF
 CC GEMIN3.
 CC -1- SUBUNIT: FORMS A STABLE HETEROOMERIC COMPLEX WITH SURVIVAL OF MOTOR
 CC NEURON PROTEIN (SMN), GEMIN2 AND GEMIN3. INTERACTS DIRECTLY WITH
 CC GEMIN3 AND WITH SEVERAL SNRNP SM CORE PROTEINS, INCLUDING B/B',
 CC D1-D3, AND E.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR. LOCALIZED IN
 CC SUBNUCLEAR STRUCTURES NEXT TO COILED BODIES, CALLED GEMS, WHICH
 CC ARE HIGHLY ENRICHED IN SPliceosomal SNRNPs AND IN THE NUCLEOLUS.
 CC -----
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CC EMBL: AF173856; AAF35283.1; -
 DR mRNA processing; Spliceosome; Nuclear protein.
 KW DOMAIN 714 735 LEUCINE-ZIPPER (POTENTIAL).
 FT SEQUENCE 1058 AA; 119989 MW; 5EE1FE2EE358D6B CRC64;
 SQ

Query Match
 Best Local Similarity 4.8%; Score 84.5; DB 1; Length 1058;
 Matches 66; Conservative 36; Mismatches 115; Indels 121; Gaps 16;

QY 63 IHPRLTPSSPKD-LQQLHFAHQGDLPVAV-LEWLTQFDASITLYEGAEISVL 117
 DB 78 LQHPVPEPSDETRWQDELFFS-VGNMPTINHTILFELSLASGLFIQ-----L 128
 QY 118 QLTNNEELCVAFEFSLKLRHHRMRRTFSHFVVDPDQE-----YEVTVH----- 162
 DB 129 LKALPTTIC-----HAELERF-LEHYVVDTSAEVAFELDIWEMVHKHGPDP 176
 QY 163 -----HLPKPT-PPGDPNHQSKNLFVPDCEHARMKVTTP----- 195
 DB 177 PLTSOFSAHAKYLPALDERPFRPKLRSDPACPTPLMLRLGLTQIQSRILGPGRK 236
 QY 196 CMSGSLW-----DPNITVETLEAHQLRVSFTLMNEST-----HYQL----- 233
 DB 237 CCALANLADMLTVFALTEDDPQEVSAIVYLDKLTAVISWNSDTQNPYHQALAEKVEA 296
 QY 234 -----LTSPFHEHNSCF---EHMHIIAPRPEFHQ-----R 263
 DB 297 ERDVSITSLAKLPSETIIVGCEFLHLLREWGEELQAVLRSSQGSYDSTRCDLSLIFS 356
 QY 264 SVNTLTLLNLKGCCHQVQIOPFESSCINDCLRHSAY 301
 DB 357 QNATILYL-NRTSLSKEDRQVVSLEACVDFLRTSTV 393

RESULT 10

INF_ANAPL STANDARD; PRT; 191 AA.

AC P51526;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 01-OCT-1996 (Rel. 34, Last annotation update)
 GN INTERFERON PRECURSOR.
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 NCBI_TaxID=8839;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=96010237; PubMed=7571434;
 RA Schulte U., Koeck J., Schlicht H.J., Staeheli P.;
 RT Recombinant duck interferon: a new reagent for studying the mode of
 RL Interferon action against hepatitis B virus.;
 Virology 212:641-649(1995).
 -I- INDUCTION: BY VIRUSES.
 -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
 FAMILY.

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DR EMBL: X84764; CAA9235.1; -
 DR HSSP: P01574; IAU1
 DR InterPro: IPR000471; -
 DR Pfam: PF00143; Interferon; 1.

DR PROSITE; P500252; INTERFERON_A-B-D; 1.
 KW Cytokine; Antiviral; Glycoprotein; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 191
 FT DISULFID 31 191
 FT DISULFID 67 167
 FT DISULFID 67 167
 FT CARBOHYD 60 154
 FT CARBOHYD 77 77
 FT CARBOHYD 161 161
 SQ SEQUENCE 191 AA; 21651 MW; 34D197AC899B82F CRC64;

Query Match
 Best Local Similarity 4.7%; Score 83; DB 1; Length 191;
 Matches 56; Conservative 29; Mismatches 70; Indels 118; Gaps 15;

QY 8 PSAPVGP-LLGILLILGLVLAAGCA-----SLRLDRAALVCSQPLNC 50
 DB 4 PSAPPPAIVSALALLILITPPANAFSCPLRLHDSAFAMDSIQLLNMAVSPTQP---C 60
 QY 51 TVKNSIC-LDQSWTHPRNLPSSPKDQQLHFAHQGDLPVAVHEWLTQFDASITLY 109
 DB 61 PQAHAPSPPTLLDITDQQAHTALHLQLHFDLSSPTP-AH-W----- 106
 QY 110 EGAEISVLQLTNNEELCVAFEFSLKLRHHRMRRTFSHFVVDPDQEYEVTVHLLPKPI 169
 DB 107 -----LHT-----ARHDLNQLQH-----IHHLEKCP 130
 QY 170 -----DQDPR-HQSKNLFVPDCEHARMKYV-TPCMSGSLMDPNITVETLEAHQLRV 219
 DB 131 ADAARLRHGRPNRLHSIKRYGCIQHLQNTYSPC-----AMD----- 170
 QY 220 SPTLMNESTHYQILITSPFHEHNSCFEHHHI 252
 DB 171 -----HVR-----LEAHACFORIHL 186

RESULT 11

RPB3_MOUSE STANDARD; PRT; 275 AA.

AC P97760;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE DNA-DIRECTED RNA POLYMERASE II 33 KDA POLYPEPTIDE (EC 2.7.7.6) (RPB3)
 DE (RNA POLYMERASE II SUBUNIT 3) (RPB33) (RPB31).
 GN POLR2C OR RP02-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97186689; PubMed=9034305;
 RA Korobko I.V., Yamamoto K., Nogai Y., Muramatsu M.;
 RT Protein interaction cloning in yeast of the mouse third largest RNA
 RL polymerase II subunit, mRPB31.;
 Gene 185:1-4(1997).
 -I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -I- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
 CC RNA(N).
 CC -I- SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
 CC -I- SUBCELLULAR LOCATION: NUCLEAR.
 CC -I- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
 CC FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
 CC PRECURSOR, POLYMERASE II FOR THE mRNA PRECURSOR, AND POLYMERASE
 CC III FOR 5S AND 5.8S rRNA GENES.
 CC -I- SIMILARITY: BELONGS TO THE RPB3/RPC5 RNA POLYMERASE SUBUNIT
 CC FAMILY.

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CC      ----- M85265; MAC36947.1.
CC      EMBL; J01290; J01290.
DR      PIR; J01290; J01290.
DR      InterPro; IPRO00728; -.
DR      InterPro; PF00586; AIRS; 2.
DR      Pfam; PF00586; AIRS; 2.
DR      Purine biosynthesis; 123
KW      112
DR      NP_BIND 740 AA; 79481 MW;
SQ      SEQUENCE
FT      Score 83; DB 1; Length 740;
       Pred. No. 12; Indels 136; Caps 20;
       ...
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CC      modified and this license agreement).
CC      entitles requires to license agreement).
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CC      ----- M85265; MAC36947.1.
CC      EMBL; M85265; JCI1290.
DR      PIR; JCI1290; JCI1290.
DR      InterPro; IPRO00728; -.
DR      pfam; PF00586; AIRS; 2.
DR      Pfam; PF00586; AIRS; 2.
DR      Purine biosynthesis; 123
KW      112
KW      NP BIND    740 AA; 79481 MW;
SQ      SEQUENCE   740 AA; 79481 MW;
FT      Score 83; DB 1; Length 740;
          Pred. No. 12; Indels 136; Caps 20;
          4.7%;
```

[illegible]

```
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE DOMAIN. BELONGS TO THE EYN/MOG SUBFAMILY.
CC -----
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CC -----
CC EMBL: AB014553; BAA31628.1; -
CC DR InterPro: IPR003006; -
CC DR Pfam: PF00047; 19; 2.
CC KW Hypothetical protein; Glycoprotein; Transmembrane;
CC Immunoglobulin domain.
CC FT NON_TER 1 1
CC FT DOMAIN 298 298 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 299 319 POTENTIAL.
CC FT DOMAIN 320 358 CTROPOLASMIC (POTENTIAL).
CC FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 558 AA: 60890 MW: 63393940F03792E1 CRC64;

Query Match
Best Local Similarity 23.0%; Score 81.5; DB 1; Length 558;
Matches 32; Conservative 13; Mismatches 57; Indels 37; Gaps 5;

QY 177 SKNPLVPCDEHAKKVTTPCMSSGMDPNTVETLEAHLRVSFTL-WNESTHYQLLT 235
DB 367 SKNF-----OKAVYPCLEQLLFLETQSPKWCARHFLQPLGLGMHFGVHTLRW 417
QY 236 SEPMENHSCFEHMHLPAPRPEEFHORSNTLLRLNKGCCRHQVOYIQPFSSCLNDCL 295
DB 418 DFPN-----HSRETSARF-----PRSPVPSDQGVGGSRH----- 450
QY 296 RHSATVSCPEMPDPPEPIP 314
DB 451 RRPAPMGCEPVQAPAPSP 469

RESULT 15
RPB3_HUMAN STANDARD; PRT; 275 AA.
AC P19387; O15161;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE II 33 KDA POLYPEPTIDE (EC 2.7.7.6) (RPB3)
DE (RNA POLYMERASE II SUBUNIT 3) (RPB33) (RPB31).
GN POLR2C OR A-152E5.7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=90256750; PubMed=2187864;
RA Part U.K., Weissman S.M.;
RT "The amino acid sequence of the human RNA polymerase II 33-kDa
RT subunit hRPB 33 is highly conserved among eukaryotes.";
RL J. Biol. Chem. 265:8400-8403(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98201707; PubMed=9540830;
RA Damman R., Pfeiffer G.P.;
RT "Cloning and characterization of the human RNA polymerase I subunit
RT hRPA40.";
RL Biochim. Biophys. Acta 1396:153-157(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Bruno T., di Padova M., de Angelis R., Iacobini C., Lovari S.,
RA Passaniti C., Fanciulli M.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99425270; PubMed=10493829;
RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
RA Fuhrman J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from
RT human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC RNA(N).
CC -1- SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
CC POLR2J AND POLR2C SUBUNITS INTERACT WITH EACH OTHER.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC III FOR 5S AND TRNA GENES.
CC -1- SIMILARITY: BELONGS TO THE RPB3/RPC5 RNA POLYMERASE SUBUNIT
CC FAMILY.
CC -----
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CC -----
CC EMBL: J05448; AAA36586.1; -
CC EMBL: AF008443; AAC14355.1; -
CC EMBL: AJ224143; CAAL1842.1; -
CC EMBL: AJ224144; CAAL1843.1; -
CC EMBL: AC004382; AAC24309.1; -
CC PIR: A36264; A36264.
CC DR MIM: 180663; -
CC DR InterPro: IPR001514; -
CC DR PROSITE: PS00446; RNA_POL_D_30KD; 1.
CC KW Transcription; DNA-directed RNA polymerase; Transcription;
CC Nuclear protein.
CC FT DOMAIN 88 97 CYS-RICH.
CC FT CONFLICT 194 194 H->T (IN REF. 1 AND 3).
CC FT SEQUENCE 275 AA: 31441 MW: EF663BE096046A4B CRC64;

Query Match
Best Local Similarity 20.3%; Score 81; DB 1; Length 275;
Matches 44; Conservative 28; Mismatches 81; Indels 64; Gaps 8;

QY 54 NSTCLDDSWI-HPRNLTTPSSPKDILQILHFAHTQGDLP-PAVHIEMTLQ----- 101
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Db 55 NSSVLHDEFIAHRLGLIFLISDDIVDKLQYSRDCTCEERCPCSVETLIDVRCNEDQTRH 114
QY 102 -TDASIL-----YLEGAELSVLQINTNERLCVREPEFLSKLRHHHR 140
Db 115 VTSRDLISNPRVLPVYTSRNRNDNDPNDYVEODDILIVKLRKGQELRLRAYAKGFGKEHA 174
QY 141 RWRFTFS-HFVVDPQEXEYVTVHLLPKPIPDG-----DPNHQSKNFL--VP 183
Db 175 KWNPTAGVAFEXYDPDNALRHVTVYPRPEEMPKSEYSELEDEDESQAPYDPNGKPERFYNVE 234
QY 184 DCEHARMKVITPCMSSGSLMDPNITVETLEAHQLRVS 220
Db 235 SC-----GSLRPETIVLSALSGIKKKLS 257

```

Search completed: July 17, 2001, 11:21:05
 Job time: 159 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 17, 2001, 11:19:56 ; Search time 26.59 Seconds
(without alignments)
916.730 Million cell updates/sec

Title: US-09-488-728-4_COPY_1_320

Perfect score: 1764

Sequence: 1 MGARSPSPSAVPGPLGLL.....VSCPEMPDPEPDPYPLM 320

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 7617452 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR:68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	5.2	593	2 H84779	hypothetical prote
2	90.5	5.1	260	2 I51544	MHC class II beta-
3	88.5	5.0	249	1 VGXRHB	glycoprotein VP7 p
4	88.5	5.0	1144	2 A54810	TMV resistance pro
5	88.5	5.0	1402	2 S42748	finger protein - f
6	88	5.0	679	2 B96599	epidermal growth f
7	88	5.0	1210	1 GQHUF	hypothetical prote
8	87.5	5.0	234	1 T43709	multifunctional am
9	87.5	5.0	1714	1 S18644	M3 protein - huma
10	86.5	4.9	771	1 JC7388	xylose isomerase (
11	86	4.9	439	1 ISHIX	dopamine beta-mono
12	86	4.9	603	2 S03020	GPI-linked recepto
13	85.5	4.8	397	2 JE0082	probable serine/ch
14	85	4.8	307	2 S62556	hypothetical prote
15	84.5	4.8	1151	2 T38424	protein-tyrosine-p
16	84.5	4.8	1442	2 S72441	hypothetical prote
17	84.5	4.8	1956	2 T00051	DNA-directed RNA p
18	84	4.8	275	2 A36264	interferon precurs
19	83	4.7	191	2 S57642	RNA polymerase II
20	83	4.7	275	2 JC6181	hypothetical prote
21	83	4.7	342	2 T48257	hypothetical prote
22	83	4.7	373	2 S54545	hypothetical prote
23	83	4.7	593	2 T19832	hypothetical prote
24	83	4.7	656	2 T21178	phosphoribosylform
25	83	4.7	741	1 JC1290	conserved hypobeth
26	82.5	4.7	1207	2 C70013	protein-tyrosine k
27	82.5	4.7	540	1 TVPVB	kinase-related tra
28	82.5	4.7	507	2 S00727	hypothetical prote
29	82.5	4.7	583	2 T30131	

30	82.5	4.7	959	2 T25704	hypothetical prote
31	82.5	4.7	2025	2 D86201	protein F12k11.6 l
32	82	4.6	448	2 S03186	lg heavy chain C r
33	81.5	4.6	288	2 C96662	lysosome-associated
34	81.5	4.6	416	1 A31959	hypothetical prote
35	81.5	4.6	1785	2 T21558	hypothetical prote
36	81.5	4.6	1929	2 T21559	hypothetical prote
37	81	4.6	329	2 S77336	hypothetical prote
38	81	4.6	732	2 D40899	pol polyprotein
39	81	4.6	2244	2 T08212	RNA-directed RNA p
40	80.5	4.6	2244	2 T08212	sugar hydrolase II
41	80.5	4.6	1164	2 E86812	DNA polymerase III
42	80.5	4.6	1197	2 G82100	sensor protein evg
43	80.5	4.6	1227	2 A86245	hypothetical prote
44	80.5	4.6	1809	2 T17403	pyochelin syntheta
45	80.5	4.6	1809	2 C83118	pyochelin syntheta

ALIGNMENTS

RESULT 1
H84779 Hypothetical protein At2g36370 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84779
R:Lin. x.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Tallon,
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Title: Sequence number: A84420; MUID:20083487
A:Reference: H84779
A:Accession: H84779
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-593 <STO>
A:Cross-references: GB:AE002093; NID:96598633; PIDN:AAF18663.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g36370
A:Map position: 2

Query Match 5.2%; Score 92; DB 2; Length 593;

Best Local Similarity 22.6%; Pred. No. 6.8; Indels 96; Gaps 15;
Matches 67; Conservative 33; Mismatches 33

QY	55	STCLDDSWIHPRNLTPSSPKDQIQLFHATQGGDLPVNAHIEWTLQTDAS-ILYLEGAE 113	
DB	182	STCLVDS-----LTGDPPTDVRVL-----TEYSEITLDSGP 214	
QY	114	LSYQLNTNINERLCVFEFLSKLHHRRWRFTSHFYVDP--DOEYEVYHHLPKPIPDG 171	
DB	215	---QINENSLL--LSLIPNSYFANLRMRKSLSEFLKPNDDDRHQDSHRTPLISF 267	
QY	172	DPNHQSKNLFVPCERAKRKVTTPCMSG-----SLMPDNTVELEHQRVFTL 223	
DB	268	E---SVKEIDISKQRUDRYVIAKCFKSPSLRKIRAYALINIKVSTL--LELLNFR 322	
QY	224	WNE-----STHY--QILLTSF-----PHMNHSCFEHMH 250	
DB	323	LTEVDLTVDSPIIPVQASVYSGOVGYTSFSENSILALCATISMTNEMDINSVASNIQ 382	
QY	251	HIPAPRPEEFHQRNVTLLRNKGCGRHOVOTOPFSSCLNDCLRHSTVSCPEMP 307	
DB	383	TLHMSKCGISSETILNLIHS-----OKMKSICLIRP-TVSDSVYLC-EFP 426	

RESULT 2
I51544 MHC class II beta-chain - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000

C:Accession: I51544
 R:Sato, K.; Flajnik, M.F.; Pasquier, L.D.; Katagiri, M.; Kasahara, M.
 J. Immunol. 150, 2831-2843, 1992
 A:Title: Evolution of the MHC: isolation of class II beta-chain cDNA clones from the Atp
 A:Reference number: I51539; MUID:93203604
 A:Accession: I51544
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-260 <SAT>
 A:Cross-references: GB:D13688; NID:9287582; PIDN:BA02845.1; PID:9287583
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
 F:130-195/Domain: immunoglobulin homology <IM>

Query Match
 Best Local Similarity 5.1%; Score 90.5; DB 2; Length 260;
 Matches 64; Conservative 34; Mismatches 97; Indels 87; Gaps 17;

QY 11 VGPPLGLLLLLGLVAGASLRLLDRAALVCSOGLN-----CFKNSCTLDDSD- 61
 DB 4 IVPVPL-CLLLTLGL-----CLCSSPEDEYVYQKGCYRNGT---DNV 44
 QY 62 ---NIPRNLPSSPKDLQIOLHFAHMOQGLDFVAHIEWTLQTDASILYLEGAEISVLO 118
 DB 45 RLKRRHYNLLEEDYEPFSDVGLFAKTGLGK--PDAD-MNNSQK---FLDQTRAAY-- 95
 QY 119 LNTVERLCVREFELSKLRHHRRMRFTFSHFVVDPRQEFVTVNHLKPIPDGDPHNSK 178
 DB 96 ---DVC-----RHNYQ-----IDKPYTID-----RKSQPNVAVI 122
 QY 179 NFIVPDCEHARMKVTTPKSSGSLMDPNTIVETL-----EAHQLRVSTLMESHVIOI- 232
 DB 123 NTKTLDEHNL---ITCEVDG-FEPPMIKVTWLNKGEISQVATSSLLDNGWMEIIN 178
 QY 233 ---LTSFPMENHSCFEMHNLIPARPEEFHORSNVTLILN 272
 DB 179 VLETTIKIGDTFTC--RVEHSSLDQPVSVNMEPDVSESARN 218

RESULT 3
 VCKRHB
 glycoprotein VP7 precursor - human rotavirus B
 C:Species: human rotavirus B
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
 C:Accession: A37080
 R:Chen, G.M.; Hung, T.; Mackow, E.R.
 Virology 178, 311-315, 1990
 A:Title: Identification of the gene encoding the group B rotavirus VP7 equivalent: prima
 A:Reference number: A37080; MUID:90357782
 A:Accession: A37080
 A:Molecule type: genomic RNA
 A:Residues: 1-249 <CHD>
 A:Cross-references: EMBL:M3872; NID:9210569; PIDN:AAA42675.1; PID:9210570
 A:Note: the authors translated the codon GAT for residue 88 as Val and GGA for residue B
 C:Genetics:
 A:Map position: segment 9
 C:Superfamily: rotavirus B glycoprotein VP7
 C:Keywords: capsid protein; glycoprotein
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-24/Product: glycoprotein VP7 #status predicted <VP7>
 F:45,91,105/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match
 Best Local Similarity 5.0%; Score 88.5; DB 1; Length 249;
 Matches 48; Conservative 30; Mismatches 82; Indels 57; Gaps 9;

QY 104 ASILYEGAEISVLOIN---INERLCVREFELSKLRHHRRMRFTFSHFVVDPRQEFV 159
 DB 2 ASILYLVLAAYVAQAQNTVPSTHPEVCVLY-----ADHQ----- 36
 QY 160 TVNHLKPIPDGDPHNSKNTLVPCDEHARMKVTTPKSS-SSSLMDPNTIVETLEAQLR 218

DB 37 -----ADANKFNGNF--TQIFHSTNLTLEFMSYSSSYD---VIDLISKYDLS 80
 QY 219 ---VSFTLWNESTHYOILLTSFPMENHSCFEMHNLIPARPEEFHORSNVTLILN 274
 DB 81 SCNTLADVENAMSDRNVFLOSTNNCSKYNA-NKVHNVKLPFGEMFYS-----KNLK 133
 QY 275 GCCRHQVQIQPFSSCLNDCLRSATVSCPEMDPPE 311
 DB 134 FCPSLSDIGMYCDTQISDTYFEISRGTYEYTDIPE 170

RESULT 4
 A54810
 TMV resistance protein N - tobacco (Nicotiana glauca)
 C:Species: Nicotiana glauca
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
 C:Accession: A54810
 R:Whitham, S.; Dinesh-Kumar, S.P.; Choi, D.; Hehl, R.; Cory, C.; Baker, B.
 Cell 78, 1101-1115, 1994
 A:Title: The product of the tobacco mosaic virus resistance gene N: similarity to tol
 A:Reference number: A54810; MUID:95007759
 A:Accession: A54810
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1144 <WHT>
 A:Cross-references: GB:U15605; NID:9558886; PIDN:AAA50763.1; PID:9558887
 C:Genetics:
 A:Gene: N
 A:Introns: 160/2; 525/3; 616/3 1139/3

Query Match
 Best Local Similarity 5.0%; Score 88.5; DB 2; Length 1144;
 Matches 44; Conservative 29; Mismatches 57; Indels 83; Gaps 12;

QY 172 DPNHOSKNFVPCDEHARMKVTTPKSSGSLM-----DNITVETLEAQLRVSEF 222
 DB 504 DPEKSRMLAKKEVEEV-MSNNTGTMAEAIWVSSYSTIRSNQAVKNMK-RLRV-FN 559
 QY 223 LWNSTHYOI-----LTSFP-----HNE-NHSCFEM-----HNHP 253
 DB 560 MGRSTHYAIDYLPNNLRGVCTNTPESFPSTELKMLVHQLRHSNLRHMTETKHP 619
 QY 254 APRPEEFHORSNVTLT---LNK-----GCCRHQVQIQPFSSCL 291
 DB 620 SLRRIDLSMKRLKRPDPTGMPNLEYVNLVYCSNLEVHNSLGGCCSKVIGLY-----L 673
 QY 292 NDC-----LRSATVSCPEMDPPE 311
 DB 674 NDCSLKRPFCVNVESLELYLGLRSCDSLKPE 706

RESULT 5
 S42748
 finger protein - fruit fly (Drosophila virilis) (fragment)
 C:Species: Drosophila virilis
 C:Date: 20-Oct-1994 #sequence_revision 26-May-1995 #text_change 24-Sep-1998
 C:Accession: S42748
 R:Schub, R.
 submitted to the EMBL Data Library, November 1993
 A:Reference number: S42748
 A:Accession: S42748
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1402 <SCH>
 A:Cross-references: EMBL:227444; NID:9426461; PID:9426462
 C:Genetics:
 A:Gene: FlyBase:FlyBase:FBgn0013137
 A:Cross-references: FlyBase:FBgn0013137
 C:Keywords: DNA binding; transcription regulation

Query Match

5.0%; Score 88.5; DB 2; Length 1402;

Best local Similarity	21.1%;	Pred. No. 38;	18
Matches	74;	Conservative	33;
		Mismatches	114;
		Indels	129;
		Gaps	54

RESULT 6
B96599
protein F20N2.12 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: B96599
R.Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, N.F.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marshall
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venturi, J.C.; Davis, R.W.
A.Title: Sequence number: AB6141; MUID:21016719
A.Reference: B96599
A.Accession: B96599
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-679 <STO>
A.Cross-references: GB:AE005173; NID:q8778489; PIDD:AAF79497.1; GSPDB:GN00141
C.Genetics:
A:Gene: F20N2.12
A:Map position: 1

[illegible]

RESULT
7
GQHFE
epidermal growth factor receptor precursor - human
N:Contains: Protein-tyrosine kinase (EC 2.7.1.112) erbB
C:Species: Homo sapiens (man)
C:Date: 15-Nov-1984 #sequence_revision 27-Nov-1985 #text_change 11-Jun-1999
C:Accession: A00641: A25772; S30024; A38672; A00642: A34615; A23062; A05281; A60143;
R:Ulrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J.
rg, P.H.
Nature 309, 418-425, 1984
A:title: Human epidermal growth factor receptor cDNA sequence and aberrant expression
A:reference number: A00641; MUID:84219729
A:Accession: A00641
A:molecule type: mRNA
A:Residues: 1-1210 <URL>
A:Residue-references: EMBL:X00588; NID:g31113; PIDN:CAA2540.1; PID:g757924
A:Notes: the authors translated the codon AAG for residue 540 as Asn
R:Inili, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 4920-4924, 1985
A:title: Characterization and sequence of the promoter region of the human epidermal
A:reference number: A25772; MUID:85270438

A:Accession: A23172
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-29 <INSH>
A:Cross-references: GB:M124; NID:g181981; PIDN:AA52370.1; PID:g553272
R: Haley, J.; Whittle, N.; Bennett, P.; Kitchington, D.; Ullrich, A.; Waterfield, M.
Oncogene Res. 1, 375-396, 1987
A:Title: The human EGF receptor gene: structure of the 110 kb locus and identification
A:Reference number: S30024; MUID:88217333
A:Accession: S30024
A:Molecule type: DNA
A:Residues: 1-29 <HA2>
A:Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119
R: Haley, J.D.; Waterfield, M.D., 1991
J. Biol. Chem. 266, 1746-1753.
A:Title: Contributory effects of de novo transcription and premature transcript termi
A:Reference number: A38672; MUID:91107677
A:Accession: A38672
A:Molecule type: DNA
A:Residues: 1-29 <HA2>
A:Cross-references: GB:M38425; NID:g181977; PIDN:AA63171.1; PID:g553271
A:Experimental source: carcinoma cell line A43-7
R: Xu, Y.; Ishii, S.; Clark, A.S.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.;
Nature 309, 806-810, 1984
A:Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RN
A:Reference number: A00642; MUID:84245835
A:Accession: A00642
A:Molecule type: mRNA
A:Residues: 'RCAMRNA', 150-187, 'KSVIOAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-
'798-799, 'TD', 802-811, 'R', 813-942 <XUV>
A:Experimental source: A431 human carcinoma cells, which have large numbers of EGF re
R: Lin, C.R.; Chen, W.S.; Krutiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma,
Science 224, 843-848, 1984
A:Title: Expression cloning of human EGF receptor complementary DNA: gene amplificatio
A:Reference number: A43615; MUID:84196372
A:Accession: A43615
A:Molecule type: mRNA
A:Residues: 713-964 <LIN>
A:Experimental source: epidermoid carcinoma cell line A431
R: Simmen, F.A.; Gope, M.L.; Schultz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, B.W.
Biochem. Biophys. Res. Commun. 124, 125-132, 1984

A:Reference number: A23062; MUID:85046483
A:Accession: A23062
A:Molecule type: mRNA
A:Residues: 1028-1210 <SIM>
R:Weber, W.; Gill, G.N.; Speiss, J.
Science 224, 294-297, 1984
A:Reference number: A05281; MUID:84172183
A:Accession: A05281
A:Molecule type: protein
A:Residues: 25-30, 'S', '32-51; 454-467 <WEB>
R:Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5208, 1985
A:Title: Identification of residues in the nucleotide binding site of the epidermal growth factor receptor
A:Reference number: A60143; MUID:85182650
A:Accession: A60143
A:Molecule type: protein
A:Residues: 740-744, 'X', '746-747 <RUS>
R:Mrzczowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A:Title: ATP-stimulated interaction between epidermal growth factor receptor and superoxide dismutase
A:Reference number: A38023; MUID:84191354
A:Accession: A38023
A:Contents: annotation; receptor activity
A:Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
R:Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J.
Cell 59, 33-43, 1989
A:Title: Functional independence of the epidermal growth factor receptor from a domain that mediates internalization
A:Reference number: A3331; MUID:90032233
A:Accession: A3331
A:Contents: annotation; internalization signal
C:Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor complex
C:Genetics:
A:Gene: GDB:EGFR
A:Cross-references: GDB:120610; OMIM:131550
A:Map position: 7p12.3-7p12.1
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphatase; signal sequence
F:24/DNA: signal sequence #status predicted <SIG>
F:25-1210/Product: EGF receptor #status predicted <MNF>
F:25-645/DNA: extracellular #status predicted <EXT>
F:75-300/DNA: EGF receptor extracellular domain repeat <EB1>
F:390-600/DNA: EGF receptor extracellular domain repeat <EB2>
F:646-668/DNA: transmembrane #status predicted <TM>
F:669-1210/DNA: intracellular #status predicted <INT>
F:710-975/DNA: intracellular #status predicted <INT>
F:718-726/DNA: protein kinase homology <KTN>
F:999-1045/Region: protein kinase ATP-binding motif
F:1047-1210/Region: coated-pit mediated internalization signal
F:128,173,352,413,444,528,603/Binding site: carbohydrate binding site: Asn (covalent) #status predicted
F:745/Active site: Lys #status experimental

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Query Match      5.0%; Score 88; DB 1; Length 1210;
Best Local Similarity 22.6%; Pred No. 35;
Matches 93; Conservative 45; Mismatches 156; Indels 118; Gaps 22;

QY 15 LGLILL-----LLGVAPGASLRLL-DHRAVLSQPGINCTV---KNSCLDD-SNIR- 64
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 777 LGLICLFYVOLITDMPGCLLDVREHKKNIGSQYLNNVCYIAKNNYLEDRLVYR 64
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 65 -----PRNLPPSSKFDLQI----- 836
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 837 DLANNVAVLKPRPOAKITDFGLAKTLAEKEKYHAESGKVPIMKMALESILHRIYHQSD 89
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 90 LEPVAHLEMTLOTQASILY--LEGAEISVLQNTNRL-----CYAFEFL----- 896
      ::| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 897 VMSYGVYVWELMTGSPRYDGIPIASELSI-LEKGERLDPQPICTIDYVIMVKKCMIDA 133
      ::| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 134 KLRHHHRMRFYTSHEVYDPDEYEYTV---HHLPKPI-----PDGDPNHQSK 955
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 956 DSKRKRELLIEESKMARPR-QRYELVIOGDEHMLSPSPDSNFRALMDEEDMDVDYDAD 178
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 179 NTLVPDCEHARMKRYT--TPCMSSGLMDPNITVETLEAHQLRV-----SF----- 221
      ::| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1015 EYLIPOOGFFSSPSRPTLLSSLSATSNSTVACIDENGLOSPRIKEDSLORYSSDPT 1074
      ::| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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-QY      222 -TLMNSTHYOILLT-----SEPHMENSCHEHMH-----TPADRPPEFHORSVYTLTL 270
Db       1075 GALTDESIDDTFLPPEYINOSVPRKPGSYQNPNYHQNPLNPAPSRPHQDPHSYAV- 1133
QY      271 RMLKGCCHNOVIOPFSSCLN---DCLRHSATVSCPMR-DTEPELPDYMP 318
Db       1134 ----GNPELTNVQP---TCVNSTFDSPAHMAQNGSHQISLDNDPYQODFFP 1178

RESULT      8
T45709
hypothetical protein FLP2.40 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cross)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C/Accession: T45709
R/ChoiJne, N.; Robert, C.; Brotlier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.,
submitted to the Protein Sequence Database, November 1999
A:/Reference number: Z23010
A:/Accession: T45709
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-234 <CHO>
A:/Cross-References: EMBL:AL32955
A:/Experimental source: cultivar Columbia; BAC clone FLP2
C:/Genetics:
A:/Map position: 3
A:/Introns: 166/3; 179/3; 208/1
A:/Note: FLP2.40

```

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Query Match          5.0%; Score 87.5; DB 2; Length 234;
Best Local Similarity 22.8%; Pred. No. 5.1;
Matches 44; Conservative 20; Mismatches 82; Indels 47; Gaps 9;

QY 122 NERLCVFEFESKLRHHRRMRRTFSEFVYVDPDQEEYEVTHMLPKPIPDGDPNHSKNFL 181
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 10 SRRICNLLIFEVKLNH-----KRLSDSDNPQ---HSAMP-----DPTRRNRNAL 52
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 182 VPDCENARKMVTTPCCSSGSLMDPNITVETTLHAHOLRYSFTLMNSTHYQILL----- 234
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 53 -----SSSSSKTRPELSSGS---PNRNTGEARGCKVKRSATILLDE---EMGLPPSGSYG 102
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 235 -----TSPFHEMNSCEFHMHIPAPPEERHQRASNTLTLLNLKGC---CRHQVQIQ 102
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 103 DPNPEPRSPPYVKQOCWEKAKIKGRDPEKRRDHLGNIVFRRLVGCPCGLCHDYHYI 162
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 285 PFF---SSQLNDG 294
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 163 PYSKGGKSTLENC 175
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 9
S18644 multifunctional amino acid--tRNA ligase (EC 6.1.1.-) - fruit fly (Drosophila melanoga
C:Species: Drosophila melanogaster
C:Accession: S18644
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Cernil, C.; Kerjan, P.; Astier, M.; Gratecos, D.; Mirande, M.; Semeriva, M.
EMBO J. 10, 4267-4277, 1991
A:Title: A component of the multisynthetase complex is a multifunctional aminoacyl-tR
A:Accession: S18644; MUID:92097547
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 11714 <CER>
A:Cross-references: GB:M74104; NID:g157563; PIDN:AAA28594.1; PID:g157564
A:Gene: FlyBase:Aats-glupro
C:Cross-references: FlyBase:Fggn0005674
C:Superfamily: Drosophila multifunctional amino acid--tRNA ligase; amino acid--tRNA l
C:Keywords: aminoacyl-tRNA synthetase; ATP; ligase; multifunctional enzyme; protein b

```


Tue Jul 17 11:27:36 2001

F:204-480/Domain: glutamine--trna ligase homology <EGL>
 F:755-800/Domain: amino acid--trna ligase repeat homology <ATL1>
 F:827-872/Domain: amino acid--trna ligase repeat homology <ATL2>
 F:901-946/Domain: amino acid--trna ligase repeat homology <ATL3>
 F:980-1025/Domain: amino acid--trna ligase repeat homology <ATL4>
 F:1055-1100/Domain: amino acid--trna ligase repeat homology <ATL5>
 F:1129-1173/Domain: amino acid--trna ligase repeat homology <ATL6>

Query Match 5.0%; Score 87.5; DB 1; Length 1714;
 Best Local Similarity 19.2%; Pred. No. 59; Indels 131; Gaps 17;
 Matches 71; Conservative 48; Mismatches 119

32 SLRLDRLALVCSQGLNCTVCSGLDSDWTHPRNLTSPSSP-----KDLQIQ-- 79
 39 SLQPPNRLVCH-----SNNVYL-----FALRAADPKYKLYGEMAIERTQIDHW 83
 80 LHFARHTQOGLFPVAHIEWTLOTDS-----LYLEGAELSYLQNTNERLCVREFELSK- 134
 84 LSFELTCEDD-----ISWLSFLTSPLEPPVYLVANKTLTADFALFENHSHRYEFLAK 137
 135 -LRHHRRMRRTFESHFVVDQDEEYTVNHLK-----PIPDGDPNHQSK 178
 138 GIPQVQVW-----YDLTQPLQLOKLOSLPBDAYKSPQSKQCTPAKGERKQEGK 192
 179 NFLVPDCEHAKRYTTPCMSSGSLM-----DPNITVETL 212
 193 FVDLGAEGKGVVREPPASGYLHIAKAKALLNOYALVCOGTLIMRPDTPAKETV 252
 213 E-----AHOLRVSTLWNESTHYOILLSPFMEHSCF--BHMHTPAPRPE-- 258
 253 EFNATVIGLEOLQIPDVFTHSYFLMDLY-----CVRLIKSKAVVDOTPEOM 305
 259 -EFHOR-----SNVTLTFLNKG-----CCRHOVOQPFSSCLNDCLRHS 298
 306 KLEERQFVESANSNSYENKLSLWEMVKGSKGONTACAKRIDM-----SSPNCQMDP 360
 299 ATVSCPEMP 307
 361 TTYRCKNEP 369

RESULT 10
 JCT388
 M83 protein - human
 C:Species: Homo sapiens (man)
 C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 01-Dec-2000
 C:Accession: JCT388
 R:Motomashi, T.; Miyoshi, S.; Osawa, M.; Eyre, H.J.; Sutherland, G.R.; Matsuda, Y.; Naka
 Biochem. Biophys. Res. Commun. 276, 244-250, 2000
 A:Title: Molecular cloning and chromosomal mapping of a novel five-span transmembrane pr
 A:Reference number: JCT388
 A:Accession: JCT388
 A:Molecule type: mRNA
 A:Residues: 1-771 <MOT>
 A:Cross-references: DDBJ:AB045292
 C:Comment: This protein, as a glycosylated cell surface protein, which belongs to a new
 its biological role is related to the T cell resting status.

A:Gene: m83
 A:Map position: 16p13.3L
 C:Keywords: extracellular protein; glycolysis; transmembrane protein

Query Match 4.9%; Score 86.5; DB 2; Length 771;
 Best Local Similarity 21.1%; Pred. No. 27; Indels 127; Gaps 15;
 Matches 75; Conservative 35; Mismatches 118
 5 RSPSNVPGPLGLLLGLVLAAGASRLLDHRAVCSQGLNCTVCSGLDSDWTHPRNLTSPSSP-----KDLQIQ-- 79
 71 RVPDQVY-----LRLVLOVSRSGAA-----CTDAEIT-----VH 101
 65 PRNLT-----SFPKDLQIOLHF-----AHTQOGLFPVAHIEWT 98

Db 102 FRSGAPVYINPLGTFSPDDTAVOPSFQVGLPSTARSNSASVNVSHAPGDWFAH----- 158
 99 TLQTDASILEGALSYLQNTNERLCVREFELSKLRHHRRMRRTFESHFVVDQDEEY 197
 159 -LPPSSQKTELGLAPTCAYVQPELVTRVVEIS-----IMEPD----- 214
 159 VTVHHLPKPIPDGDPNHQSK-KNPLVPDCEHAKRYTTPCMSSGSLMDP-NITV--ETLEA 250
 198 -----VPLPQTLISHPSYLKVPDPTRELLRLRCVNSGSLGCPVRLTGPVTLPS 268
 215 HOLRVSTLWNESTHYOILLSPFMEHSCFHHHTPAPRPEEFHORSNVTL----- 291
 251 NFQKV-LTCTGAPPCPLL-----PSPMDNMLQVTAESILVPLGT 319
 269 -----TLRNKCCCRHOVOIOPESSCLNDCLRHSATVSCPEMPDPERIPDXMPL 338
 292 VAFSAVALTACRPSRVVQPLLOSQNSQNSGSLSPS-----PDHDL 338

RESULT 11
 ISHX
 xylose isomerase (EC 5.3.1.5) - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence_revision 06-Dec-1996 #text_change 18-Jun-1999
 C:Accession: D64183
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirsch, E.F.; Kerlavage
 C:Accession: D64183
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirsch, E.F.; Kerlavage
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: D64183
 A:Accession: D64183
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-439 <TIGR>
 A:Cross-references: GB:U52791; GB:I42023; NID:q1574662; PIDN:ANC22766.1; PID:q1574666
 C:Genetics:
 A:Gene: xylA
 A:Map position: FOR1177317-1178636
 A:Function: catalyzes isomerization of the aldopentose D-xylose to the 2-ketopento
 A:Description: catalyzes isomerization of the aldopentose D-xylose to the 2-ketopento
 A:Pathway: xylose metabolism
 C:Superfamily: xylose isomerase
 C:Keywords: Intramolecular oxidoreductase; isomerase; magnesium; xylose metabolism
 P:101,104/Active site: His, Asp #status predicted
 F:141,234/Binding site: substrate (Thr, Lys) #status predicted
 F:141,234/Binding site: substrate (Glu, Glu, Asp, Asp) #status predicted
 F:232,268,296,339/Binding site: magnesium (Glu, His, Asp, Asp)
 F:268,271,307,309/Binding site: magnesium (Glu, His, Asp, Asp)

Query Match 4.9%; Score 86; DB 1; Length 439;
 Best Local Similarity 20.6%; Pred. No. 15; Indels 76; Gaps 10;
 Matches 47; Conservative 34; Mismatches 71
 76 LQTLQFAHT-----QOGLFPVAHIEWTLOTDSILEGALSYLQNTNERLCVREFEL 132
 42 LRLAVCWHTFECWNGDMGLSLERSMKNSNL--LAGA-----OKADIAPFL 90
 133 SKLRHHRRMRRTFESHFVVDPP-----OEYEVVHLLPPIPDGDPNHQSKNFLVPDCEHA 188
 91 NKLGVPY-----YCFHVDVDAPEGNSVREYVONFHH-----YDILIERK 129
 189 RMKV-----TTPCMSSGSLMDPNTVETLEAHL-----RVSEFTLAN 225
 130 QVETGVKLLMGTCNCTNPRMSGATNPPEVFAAATOVFNANANATORLOGENVYVLMG 189
 226 ESTHVOILLTSPFMEHNS-----CFEHHHHP-----APRDEE 259
 190 GREGETILLNDIDKREEROIGRFQMVVEHKKIGFAGTLLIPKPOE 237

RESULT 12

S03020

dopamine beta-monoxygenase (EC 1.14.17.1) precursor - human
 M:Alternate names: dopamine beta-hydroxylase
 C:Species: Homo sapiens (man)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999

R:Kobayashi, K.; Kurohara, Y.; Fujita, K.; Nagatsu, T.
 Nucleic Acids Res. 17, 1089-1102, 1989
 A>Title: Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-terminal

A:Accession: S03020; MUID:89160241
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-603 <KOB>

A:Cross-references: EMBL:X13255; NID:g30473; PIDN:CAA1631.1; PID:g30474
 A>Note: 304-Ser and 535-Cys were also found; the amino acid exchange at residue 535 was
 R:Lamoureux, A.; Vignu, A.; Biguet, N.F.; Darmon, M.C.; Franck, R.; Henry, J.P.; Mallet,
 EMBL J. 6, 3931-3937, 1987
 A>Title: The primary structure of human dopamine-beta-hydroxylase: insights into the rel

A:Reference number: S06283; MUID:88166633
 A:Accession: S06283
 A:Molecule type: mRNA
 A:Residues: 1-196, 'T', 198-534, 'C', 536-603 <LAM>

A:Cross-references: EMBL:Y00096; NID:g30455; PIDN:CAA68285.1; PID:g30456
 A>Note: Part of this sequence was confirmed by protein sequencing
 R:Li, B.; Tsing, S.; Kosaka, A.H.; Nguyen, B.; Osen, E.G.; Bach, C.; Chan, H.; Barnett,

Biochem. J. 313, 57-64, 1996
 A>Title: Expression of human dopamine beta-hydroxylase in Drosophila Schneider 2 cells.
 A:Reference number: S61362; MUID:96132606
 A:Accession: S61362
 A:Molecule type: protein

C:Superfamily: peptidylglycine monoxygenase I homology
 F:1-23/Domain: catecholamine biosynthesis; copper; glycoprotein; monoxygenase; oxidoreduct
 F:26-603/Product: dopamine beta-hydroxylase #status predicted <SIG>
 F:282-505/Domain: peptidylglycine monoxygenase I homology <POM>

Query Match
 Best Local Similarity 4.9%; Score 86; DB 2; Length 603;
 Matches 54; Conservative 42; Mismatches 110; Indels 72; Gaps 14;

QY 68 LTPSPKDIQIOLFAHTQGDLPVANHETL-----QTDASILY----- 108
 Db 23 LQGSAPRESPLPHIPDPSGL-----ELSMVSYTQEAHHPOLLVRKAGVLFMSDR 78

QY 109 --LEGAELSTLQNTNERLCVREFELSKLRHRRRTFTSFVVDPDQEEV-TVVHILP 165
 Db 79 GELEMDLVLTWD-----GDTAYRADMSDQKQIHLDPOODYOLLOVOVOTRTP 126

QY 166 -----KPIDGDPNHSKNTFLVPCMSGSLMPDNTVELLEHQL 217
 Db 127 EELTLLEKRFECTDP-----KDYLED-----GVHVLVYGLLEPRFSLAINGSL 174

QY 218 RVSTLIMNESTHYOILLSPFHM--NHSEFENHNIAPRPRPEFHQRSVNTLTENL-K 274
 Db 175 QMGL-----QROVLKPNIPPEPLPSDAC--TMEVQANINIDIPSOETTYWYIKELPK 225

QY 275 GCGCHQ-VQLOPFSSGLINDLRHSATVSC-PRMPPTP 310
 Db 226 GFSRHILIKTEPIVTKGNELVHMEVFQCAPRMDSV 263

RESULT 13
 JE0082

GPI-linked receptor precursor - mouse
 M:Alternate names: GFRalpha-3
 C:Species: Mus musculus (house mouse)
 C:Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 02-Jun-2000

C:Accession: JE0082
 R:Nomoto, S.; Ito, S.; Yang, L.X.; Kluhl, K.

Biochem. Biophys. Res. Commun. 244, 849-853, 1998
 A>Title: Molecular cloning and expression analysis of GFRalpha-3, a novel cDNA related

A:Reference number: JE0082; MUID:98205811
 A:Accession: JE0082
 A:Molecule type: mRNA
 A:Residues: 1-397 <NOM>

A:Cross-references: DBJ:AB008833; NID:g2627159; PIDN:BAA23562.1; PID:g2627160
 C:Comment: This protein plays a distinct role in cell survival and differentiation.
 C:Superfamily: Mus musculus GPI-linked receptor
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:380-397/Region: hydrophobic
 F:92,145,306/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match
 Best Local Similarity 4.8%; Score 85.5; DB 2; Length 397;
 Matches 82; Conservative 28; Mismatches 123; Indels 99; Gaps 19;

QY 1 MGAARSPSAVPGILGLILLGLVLAAPGASRLIDHRALV--OSPGGLNCTYKNSCTL 58
 Db 1 MGLTSMSPRP-----PLMTLLVLTSLMLPLGAGNSLATERNFVNSTQARKKCEA-NPAC- 54

QY 59 DDSWIHPRNLTSPSPKDIQIOLFAHTQGDLPVANHETLQTDASTLYLEGAELSLVQ 118
 Db 55 KAVQHILGCTSLSLRPLPLE-----ESMSADC-----LEAAE-----Q 89

QY 119 LTNNEFLCVREFELSKLRHRRRTFTSFVVDPDQEEV-TVVHILP 164
 Db 90 LNNSLILDKC-----HRRKHQATCIDITWTVPARSGDELYDPEDVITSK 140

QY 165 KPIDGDPNHSKNTFLVPCMSGSLMPDNTVELLEHQL 217
 Db 141 PKM-----NLSKIMLAKPDSDLCKFAMLCITLHDCDRLRKATGAC--SIRCOHILC 193

QY 209 VETLEAHQLRVSTLIMNESTHYOILLSPFHMENHSCFENHNIAPR--PEEFHQRSN 265
 Db 194 LA-----QLNSFEKAEF--HAQGLLCPCAPDAGCGERRRNTTAPSCALP-----S 240

QY 266 VTTLRLNKGCCRHQVOIOPFSSGLINDLRH 297
 Db 241 VTPNCLDLRSFCR--ADPLCRSLMDPQTH 268

RESULT 14
 S62556
 probable serine/threonine protein kinase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000
 C:Accession: S62556; T38338
 R:Odell, C.; Churcher, C.M.
 submitted to the EMBL Data Library, November 1995

A:Reference number: S62546
 A:Accession: S62556
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-607 <ODP>

A:Cross-references: EMBL:Z67757; NID:g1061288; PIDN:CAA91776.1; PID:g1061299
 R:Odell, C.; Churcher, C.M.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, November 1995
 A:Accession: T38338
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-607 <OD2>
 A:Cross-references: EMBL:Z67757; PIDN:CAA91776.1; GSPDB:GN00066; SPDB:SPAC24B11.11c
 A:Experimental source: strain 972n-; cosmid c24B11
 A:Gene: SPAC24B11.11c
 A:Map position: 11
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

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Tue Jul 17 11:27:35 2001

us-09-488-728-4_copy_1_320.ra1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 17, 2001, 11:19:22 ; Search time 21.86 Seconds
(without alignments)
294.889 Million cell updates/sec

Title: US-09-488-728-4_COPY_1_320
Perfect score: 1764
Sequence: 1 MGAARSPPSAVPPIGLILL.....VSCPEMDPEPIPIPYMLPM 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 segs, 20144635 residues
Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents - AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfilest1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1764	100.0	866	2	US-08-620-694A-10
2	1764	100.0	866	3	US-09-022-255-10
3	1764	100.0	866	3	US-09-022-696-10
4	1764	100.0	866	3	US-08-978-773-4
5	1764	100.0	866	3	US-09-022-253-10
6	1764	100.0	866	3	US-09-022-260-10
7	1764	100.0	866	4	US-09-022-257-10
8	1764	100.0	866	4	US-09-022-257-10
9	1254	71.1	864	2	US-08-620-694A-2
10	1254	71.1	864	3	US-09-022-255-2
11	1254	71.1	864	3	US-08-978-773-2
12	1254	71.1	864	3	US-09-022-253-2
13	1254	71.1	864	3	US-09-022-260-2
14	1254	71.1	864	4	US-09-022-259-2
15	1254	71.1	864	4	US-09-022-257-2
16	1254	71.1	864	4	US-08-310-912A-108
17	88.5	5.0	1143	5	PCT-US95-04589-108
18	88.5	5.0	1144	5	US-08-261-663A-2
19	88.5	5.0	1144	1	US-08-261-663A-4
20	88.5	5.0	1144	1	PCT-US95-07754A-2
21	88.5	5.0	1144	5	PCT-US95-07754A-4
22	88.5	5.0	1210	2	US-08-475-035-4
23	88	5.0	1210	2	US-08-484-438-7
24	84.5	4.6	410	1	US-08-073-807A-16
25	81.5	4.6	353	1	US-08-073-807A-17
26	81.5	4.6	380	1	US-08-073-807A-18
27	81.5	4.6	380	1	US-08-073-807A-18

28	81.5	4.6	416	1	US-08-073-807A-2	Sequence 2, Appl1
29	81.5	4.6	1144	3	US-08-930-996A-9	Sequence 9, Appl1
30	79	4.5	671	6	5266464-2	Patent No. 5266464
31	78.5	4.5	337	5	PCT-US94-14277-8	Sequence 8, Appl1
32	78.5	4.5	1213	1	US-08-188-582-20	Sequence 20, Appl1
33	78.5	4.5	1213	1	US-08-646-715-20	Sequence 20, Appl1
34	77.5	4.4	368	1	US-08-211-942-17	Sequence 17, Appl1
35	77	4.4	459	6	5194375-2	Patent No. 5194375
36	76.5	4.3	169	3	US-08-630-172-11	Sequence 11, Appl1
37	76.5	4.3	954	2	US-08-749-169A-3	Sequence 3, Appl1
38	76.5	4.3	954	2	US-09-130-032A-3	Sequence 2, Appl1
39	76	4.3	429	5	US-07-964-589-2	Sequence 2, Appl1
40	75.5	4.3	1626	2	US-08-771-602D-2	Sequence 2, Appl1
41	75.5	4.3	1626	4	US-09-232-446B-2	Sequence 2, Appl1
42	75.5	4.3	839	1	US-08-087-016-2	Sequence 2, Appl1
43	75	4.2	399	4	US-09-284-033-2	Sequence 2, Appl1
44	74.5	4.2	399	4	US-08-729-834B-2	Sequence 2, Appl1
45	74.5	4.2	399	4	US-08-729-834B-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-620-694A-10
Sequence 10, Application US/08620694A
Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Springs, Melanle
APPLICANT: Panslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-620-694A-10

Query Match
Best Local Similarity 100.0%; Score 1764; DB 2; Length 866;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAARSPSPAVPGPLGLGILLGLVLAAGASLRLLDHRALVCSQPGINCTVKNSTCLDD 60
DB 1 MGAARSPSPAVPGPLGLGILLGLVLAAGASLRLLDHRALVCSQPGINCTVKNSTCLDD 60
QY 61 SMHPRNLTSSPKDLOQLHFAHTQOGDLEPPVAHIEMTLQTDASTILYLEGAEISVLQIN 120
DB 61 SMHPRNLTSSPKDLOQLHFAHTQOGDLEPPVAHIEMTLQTDASTILYLEGAEISVLQIN 120
QY 121 TNERLCVREFEFLSKLRHHRRMRFTHSHFYVDDPDQEVVHHLPRIPDGDPNHOSKNF 180
DB 121 TNERLCVREFEFLSKLRHHRRMRFTHSHFYVDDPDQEVVHHLPRIPDGDPNHOSKNF 180
QY 181 LVPDCEHARKKVTTPCMSSGSLMDPNITVETLEAHQLRVSTLMNESTHYOILTSFPHM 240
DB 181 LVPDCEHARKKVTTPCMSSGSLMDPNITVETLEAHQLRVSTLMNESTHYOILTSFPHM 240
QY 241 ENHSCFEHMHIIAPRPEEFHORSNVTTLRLNLKGCCHQVOIQPFSSCLNDCLRHSAT 300
DB 241 ENHSCFEHMHIIAPRPEEFHORSNVTTLRLNLKGCCHQVOIQPFSSCLNDCLRHSAT 300
QY 301 VSCPEMDTPPEPIPDYMLM 320
DB 301 VSCPEMDTPPEPIPDYMLM 320

RESULT 2

US-09-022-255-10
Sequence 10, Application US/09022255
Patent No. 6072033

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: No. 6072033e1 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)587-0430
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-10

Query Match
Best Local Similarity 100.0%; Score 1764; DB 3; Length 866;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAARSPSPAVPGPLGLGILLGLVLAAGASLRLLDHRALVCSQPGINCTVKNSTCLDD 60
DB 1 MGAARSPSPAVPGPLGLGILLGLVLAAGASLRLLDHRALVCSQPGINCTVKNSTCLDD 60
QY 61 SMHPRNLTSSPKDLOQLHFAHTQOGDLEPPVAHIEMTLQTDASTILYLEGAEISVLQIN 120
DB 61 SMHPRNLTSSPKDLOQLHFAHTQOGDLEPPVAHIEMTLQTDASTILYLEGAEISVLQIN 120
QY 121 TNERLCVREFEFLSKLRHHRRMRFTHSHFYVDDPDQEVVHHLPRIPDGDPNHOSKNF 180
DB 121 TNERLCVREFEFLSKLRHHRRMRFTHSHFYVDDPDQEVVHHLPRIPDGDPNHOSKNF 180
QY 181 LVPDCEHARKKVTTPCMSSGSLMDPNITVETLEAHQLRVSTLMNESTHYOILTSFPHM 240
DB 181 LVPDCEHARKKVTTPCMSSGSLMDPNITVETLEAHQLRVSTLMNESTHYOILTSFPHM 240
QY 241 ENHSCFEHMHIIAPRPEEFHORSNVTTLRLNLKGCCHQVOIQPFSSCLNDCLRHSAT 300
DB 241 ENHSCFEHMHIIAPRPEEFHORSNVTTLRLNLKGCCHQVOIQPFSSCLNDCLRHSAT 300
QY 301 VSCPEMDTPPEPIPDYMLM 320
DB 301 VSCPEMDTPPEPIPDYMLM 320

RESULT 3

US-09-022-696-10
Sequence 10, Application US/09022696
Patent No. 6072037

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: No. 6072037e1 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B

Tue Jul 17 11:27:35 2001

us-09-488-728-4_copy_1_320.ral

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 866 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-022-696-10

Query Match 100.0%; Score 1764; DB 3; Length 866;
 Best Local Similarity 100.0%; Pred. No. 8.9e-177; Indels 0; Gaps 0;
 Matches 320; Conservative 0; Mismatches 0;

QY 1 MGAARPPSAVPGPILGLILLGLVLAAPGASLRLLDHRALVCSOPGLNCTVKNSTCIDD 60
 |||||||
 DB 1 MGAARPPSAVPGPILGLILLGLVLAAPGASLRLLDHRALVCSOPGLNCTVKNSTCIDD 60
 |||||||

QY 61 SWIHPNLTSPSSPKDQIQLFHATQOGDLFPVAHIEMTLOTDSILYLEGAEISVLQIN 120
 |||||||
 DB 61 SWIHPNLTSPSSPKDQIQLFHATQOGDLFPVAHIEMTLOTDSILYLEGAEISVLQIN 120
 |||||||

QY 121 TNERLCVREFEFLSKLRHHRMRFTFSHFVVDPODEYEVYHHLKPIPDGDPNHOSKNF 180
 |||||||
 DB 121 TNERLCVREFEFLSKLRHHRMRFTFSHFVVDPODEYEVYHHLKPIPDGDPNHOSKNF 180
 |||||||

QY 181 LVPDCEHARKMTPTPCSSGSLMDPNITVETLEAHQLRVSTLMNESHYOILLTSPPHM 240
 |||||||
 DB 181 LVPDCEHARKMTPTPCSSGSLMDPNITVETLEAHQLRVSTLMNESHYOILLTSPPHM 240
 |||||||

QY 241 ENHSCFEHMHIPARPEEFHORSNVTLLRNKGCRRHOVOIQPFSSCLNDCLRHSAT 300
 |||||||
 DB 241 ENHSCFEHMHIPARPEEFHORSNVTLLRNKGCRRHOVOIQPFSSCLNDCLRHSAT 300
 |||||||

QY 301 VSCPEMDPTPEPIPDYPLM 320
 |||||||
 DB 301 VSCPEMDPTPEPIPDYPLM 320
 |||||||

RESULT 4
 US-08-978-773-4
 Sequence 4, Application US/08978773
 Patent No. 6083906
 GENERAL INFORMATION:
 APPLICANT: Troutt, Anthony
 TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple PowerMacintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/978,773
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 60/052,525
 FILING DATE: 27 NOVEMBER 1996
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2623-A

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 866 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-978-773-4

Query Match 100.0%; Score 1764; DB 3; Length 866;
 Best Local Similarity 100.0%; Pred. No. 8.9e-177; Indels 0; Gaps 0;
 Matches 320; Conservative 0; Mismatches 0;

QY 1 MGAARPPSAVPGPILGLILLGLVLAAPGASLRLLDHRALVCSOPGLNCTVKNSTCIDD 60
 |||||||
 DB 1 MGAARPPSAVPGPILGLILLGLVLAAPGASLRLLDHRALVCSOPGLNCTVKNSTCIDD 60
 |||||||

QY 61 SWIHPNLTSPSSPKDQIQLFHATQOGDLFPVAHIEMTLOTDSILYLEGAEISVLQIN 120
 |||||||
 DB 61 SWIHPNLTSPSSPKDQIQLFHATQOGDLFPVAHIEMTLOTDSILYLEGAEISVLQIN 120
 |||||||

QY 121 TNERLCVREFEFLSKLRHHRMRFTFSHFVVDPODEYEVYHHLKPIPDGDPNHOSKNF 180
 |||||||
 DB 121 TNERLCVREFEFLSKLRHHRMRFTFSHFVVDPODEYEVYHHLKPIPDGDPNHOSKNF 180
 |||||||

QY 181 LVPDCEHARKMTPTPCSSGSLMDPNITVETLEAHQLRVSTLMNESHYOILLTSPPHM 240
 |||||||
 DB 181 LVPDCEHARKMTPTPCSSGSLMDPNITVETLEAHQLRVSTLMNESHYOILLTSPPHM 240
 |||||||

QY 241 ENHSCFEHMHIPARPEEFHORSNVTLLRNKGCRRHOVOIQPFSSCLNDCLRHSAT 300
 |||||||
 DB 241 ENHSCFEHMHIPARPEEFHORSNVTLLRNKGCRRHOVOIQPFSSCLNDCLRHSAT 300
 |||||||

QY 301 VSCPEMDPTPEPIPDYPLM 320
 |||||||
 DB 301 VSCPEMDPTPEPIPDYPLM 320
 |||||||

RESULT 5
 US-09-022-253-10
 Sequence 10, Application US/09022253
 Patent No. 6096305
 GENERAL INFORMATION:
 APPLICANT: Yao, Zhenpin
 APPLICANT: Spriggs, Melanie
 APPLICANT: Fanslow, William
 TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/022,253
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/620,694
 FILING DATE: 21-MARCH-1996
 APPLICATION NUMBER: USSN 08/538,765
 FILING DATE: 7 AUGUST 1995
 CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)587-0430
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-253-10

Query Match
Best Local Similarity 100.0%; Score 1764; DB 3; Length 866;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARSPSAVPGPLGILLGLGYLAPGASLRDLDRALVCSQPGINCTYKNSCTCDD 60
DB 1 MGARSPSAVPGPLGILLGLGYLAPGASLRDLDRALVCSQPGINCTYKNSCTCDD 60
QY 61 SWIHPRLTPSSPKDQIQIHFATQOGDLFPVAHIEWTLQTDASITYLEGALSVLQIN 120
DB 61 SWIHPRLTPSSPKDQIQIHFATQOGDLFPVAHIEWTLQTDASITYLEGALSVLQIN 120
QY 121 TNERLCVREFEFLSKLRHHRMRFTSFHYVDPDQEVTVNHLPRIPDGPNNHOSKNF 180
DB 121 TNERLCVREFEFLSKLRHHRMRFTSFHYVDPDQEVTVNHLPRIPDGPNNHOSKNF 180
QY 181 LVPDCEHARKVTPPCSSGSLMDPNITVETLEAHQLRVSTLNNSTHYQILLTSFPHM 240
DB 181 LVPDCEHARKVTPPCSSGSLMDPNITVETLEAHQLRVSTLNNSTHYQILLTSFPHM 240
QY 241 ENHSCFEHMHITAPRPEEFHORSNVTLLRLKGCCHQVOIQPFSSCLNDCLRHSAF 300
DB 241 ENHSCFEHMHITAPRPEEFHORSNVTLLRLKGCCHQVOIQPFSSCLNDCLRHSAF 300
QY 301 VSCPEMPDTPPEPIPDYMLW 320
DB 301 VSCPEMPDTPPEPIPDYMLW 320

RESULT 6
US-09-022-260-10
Sequence 10, Application US/09022260
Patent No. 6100235
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: Fanslow, William
NUMBER OF SEQUENCES: No. 6100235e1 Receptor That Binds IL-17
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)587-0430
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-260-10

Query Match
Best Local Similarity 100.0%; Score 1764; DB 3; Length 866;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARSPSAVPGPLGILLGLGYLAPGASLRDLDRALVCSQPGINCTYKNSCTCDD 60
DB 1 MGARSPSAVPGPLGILLGLGYLAPGASLRDLDRALVCSQPGINCTYKNSCTCDD 60
QY 61 SWIHPRLTPSSPKDQIQIHFATQOGDLFPVAHIEWTLQTDASITYLEGALSVLQIN 120
DB 61 SWIHPRLTPSSPKDQIQIHFATQOGDLFPVAHIEWTLQTDASITYLEGALSVLQIN 120
QY 121 TNERLCVREFEFLSKLRHHRMRFTSFHYVDPDQEVTVNHLPRIPDGPNNHOSKNF 180
DB 121 TNERLCVREFEFLSKLRHHRMRFTSFHYVDPDQEVTVNHLPRIPDGPNNHOSKNF 180
QY 181 LVPDCEHARKVTPPCSSGSLMDPNITVETLEAHQLRVSTLNNSTHYQILLTSFPHM 240
DB 181 LVPDCEHARKVTPPCSSGSLMDPNITVETLEAHQLRVSTLNNSTHYQILLTSFPHM 240
QY 241 ENHSCFEHMHITAPRPEEFHORSNVTLLRLKGCCHQVOIQPFSSCLNDCLRHSAF 300
DB 241 ENHSCFEHMHITAPRPEEFHORSNVTLLRLKGCCHQVOIQPFSSCLNDCLRHSAF 300
QY 301 VSCPEMPDTPPEPIPDYMLW 320
DB 301 VSCPEMPDTPPEPIPDYMLW 320

RESULT 7
US-09-022-259-10
Sequence 10, Application US/09022259
Patent No. 619104
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: Fanslow, William
NUMBER OF SEQUENCES: No. 6191104e1 Receptor That Binds IL-17
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:

Tue Jul 17 11:27:35 2001

us-09-488-728-4_copy_1_320.rat

MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 CURRENT APPLICATION DATA: US/09/022,259

APPLICATION NUMBER: US/09/022,259
 FILING DATE:
 CLASSIFICATION:
 APPLICATION NUMBER: 08/620,694

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/620,694
 FILING DATE:
 CLASSIFICATION:
 APPLICATION NUMBER: USSN 08/410,535

ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 866 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-022-259-10

Query Match 100.0%; Score 1764; DB 4; Length 866;
 Best Local Similarity 100.0%; Pred. No. 8,9e-177; Indels 0; Gaps 0;
 Matches 320; Conservative 0; Mismatches 0;

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OY 1 MGAARSPSPAVPGPLGLLLGLLLGLVAPGASLRLLDHRALVCSQGLNCTVKNSTCLDD 60
Db 1 MGAARSPSPAVPGPLGLLLGLLLGLVAPGASLRLLDHRALVCSQGLNCTVKNSTCLDD 60
OY 61 SWIHRNLTPSSPKDLOIOLHFAHTQGDLPFAHIEWTLQTDASILYEGAEISVQLN 120
Db 61 SWIHRNLTPSSPKDLOIOLHFAHTQGDLPFAHIEWTLQTDASILYEGAEISVQLN 120
OY 121 TNERLCVREFELSKLRHHRMRFTFSHFVYDDPEYEVTHLPRIPDGDPNHOSKNF 180
Db 121 TNERLCVREFELSKLRHHRMRFTFSHFVYDDPEYEVTHLPRIPDGDPNHOSKNF 180
OY 181 LVPDCENARKVTPCMSSGLMDPNITVEITLHOLRVSTLAMESTHYQLLTSFPHM 240
Db 181 LVPDCENARKVTPCMSSGLMDPNITVEITLHOLRVSTLAMESTHYQLLTSFPHM 240
OY 241 ENHSCFEHMHIPAPRPEEFHORSNVTLLRLNKGCCRHQVOIOFPFSSCLNCLRSAT 300
Db 241 ENHSCFEHMHIPAPRPEEFHORSNVTLLRLNKGCCRHQVOIOFPFSSCLNCLRSAT 300
OY 301 VSCPEMPDTPPEIPDYMLW 320
Db 301 VSCPEMPDTPPEIPDYMLW 320

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RESULT 8
 US-09-022-257-10
 ; Sequence 10, Application US/09022257

Patent No. 6197525
 GENERAL INFORMATION:
 APPLICANT: Yao, Zhengbin
 APPLICANT: Spriggs, Melanie
 APPLICANT: Fanslow, William
 TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESS: Immunex Corporation

STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 CURRENT APPLICATION DATA: US/09/022,257

APPLICATION NUMBER: US/09/022,257
 FILING DATE:
 CLASSIFICATION:
 APPLICATION NUMBER: 08/620,694

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/620,694
 FILING DATE:
 CLASSIFICATION:
 APPLICATION NUMBER: USSN 08/410,535

ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 866 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-022-257-10

Query Match 100.0%; Score 1764; DB 4; Length 866;
 Best Local Similarity 100.0%; Pred. No. 8,9e-177; Indels 0; Gaps 0;
 Matches 320; Conservative 0; Mismatches 0;

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OY 1 MGAARSPSPAVPGPLGLLLGLLLGLVAPGASLRLLDHRALVCSQGLNCTVKNSTCLDD 60
Db 1 MGAARSPSPAVPGPLGLLLGLLLGLVAPGASLRLLDHRALVCSQGLNCTVKNSTCLDD 60
OY 61 SWIHRNLTPSSPKDLOIOLHFAHTQGDLPFAHIEWTLQTDASILYEGAEISVQLN 120
Db 61 SWIHRNLTPSSPKDLOIOLHFAHTQGDLPFAHIEWTLQTDASILYEGAEISVQLN 120
OY 121 TNERLCVREFELSKLRHHRMRFTFSHFVYDDPEYEVTHLPRIPDGDPNHOSKNF 180
Db 121 TNERLCVREFELSKLRHHRMRFTFSHFVYDDPEYEVTHLPRIPDGDPNHOSKNF 180
OY 181 LVPDCENARKVTPCMSSGLMDPNITVEITLHOLRVSTLAMESTHYQLLTSFPHM 240
Db 181 LVPDCENARKVTPCMSSGLMDPNITVEITLHOLRVSTLAMESTHYQLLTSFPHM 240
OY 241 ENHSCFEHMHIPAPRPEEFHORSNVTLLRLNKGCCRHQVOIOFPFSSCLNCLRSAT 300
Db 241 ENHSCFEHMHIPAPRPEEFHORSNVTLLRLNKGCCRHQVOIOFPFSSCLNCLRSAT 300
OY 301 VSCPEMPDTPPEIPDYMLW 320
Db 301 VSCPEMPDTPPEIPDYMLW 320

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RESULT 9
 US-08-620-694A-2
 ; Sequence 2, Application US/08620694A

Patent No. 5869286
 GENERAL INFORMATION:
 APPLICANT: Yao, Zhengbin

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us-09-488-728-4_copy_1_320.ra1

APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286e1 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immune Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)587-0430
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-620-694A-2

Query Match
Best Local Similarity 71.1%; Score 1254; DB 2; Length 864;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;
QY 1 MGAARPSAVPGPLGLLLGLVAPGASRLDHRALVCSOGLNCTKNSCTCDD 60
DB 1 MAIRCRPRVYVPGALGMLLLNLVAPGRASPRLLDFPAPVCAQEGISCRVKNSTCDD 60
QY 61 SWIHRNLTPSSPRDLOIOLHFAHQOGLDFPAHIEWTLOTDAISILYLEGAEISVLOLN 120
DB 61 SWIHRNLTPSSPRDLOIOLHFAHQOGLDFPAHIEWTLOTDAISILYLEGAEISVLOLN 120
QY 121 TNERLCVREFELSKLHNRHRRFTFSHFVVDPOEYEVVHNLPRIPDGDNRHNSKMF 180
DB 121 TNERLCVREFELSKLHNRHRRFTFSHFVVDPOEYEVVHNLPRIPDGDNRHNSKMF 180
QY 181 LVPDCEHARKVYTPCMSSGSLMDPNITVEITLRAHQLRVSTLMESTHYQLTSPFHM 240
DB 181 LVPDCEHARKVYTPCMSSGSLMDPNITVEITLRAHQLRVSTLMESTHYQLTSPFHM 240
QY 241 ENHSCFEMHHHPAPRPEEFHORSNTLTLLRLKGCCHROVOYIOFFSSCINDCLRSAT 300
DB 241 ENHSCFEMHHHPAPRPEEFHORSNTLTLLRLKGCCHROVOYIOFFSSCINDCLRSAT 300
QY 301 VSCPEMDPT--PEPIDVYALM 320
DB 301 VPCPVISNTTVKRPVADITPLM 320

RESULT 10
US-09-022-255-2
Sequence 2, Application US/09022255
Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: No. 6072033e1 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immune Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)587-0430
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-2

Query Match
Best Local Similarity 71.1%; Score 1254; DB 3; Length 864;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;
QY 1 MGAARPSAVPGPLGLLLGLVAPGASRLDHRALVCSOGLNCTKNSCTCDD 60
DB 1 MAIRCRPRVYVPGALGMLLLNLVAPGRASPRLLDFPAPVCAQEGISCRVKNSTCDD 60
QY 61 SWIHRNLTPSSPRDLOIOLHFAHQOGLDFPAHIEWTLOTDAISILYLEGAEISVLOLN 120
DB 61 SWIHRNLTPSSPRDLOIOLHFAHQOGLDFPAHIEWTLOTDAISILYLEGAEISVLOLN 120
QY 121 TNERLCVREFELSKLHNRHRRFTFSHFVVDPOEYEVVHNLPRIPDGDNRHNSKMF 180
DB 121 TNERLCVREFELSKLHNRHRRFTFSHFVVDPOEYEVVHNLPRIPDGDNRHNSKMF 180
QY 181 LVPDCEHARKVYTPCMSSGSLMDPNITVEITLRAHQLRVSTLMESTHYQLTSPFHM 240
DB 181 LVPDCEHARKVYTPCMSSGSLMDPNITVEITLRAHQLRVSTLMESTHYQLTSPFHM 240
QY 241 ENHSCFEMHHHPAPRPEEFHORSNTLTLLRLKGCCHROVOYIOFFSSCINDCLRSAT 300
DB 241 ENHSCFEMHHHPAPRPEEFHORSNTLTLLRLKGCCHROVOYIOFFSSCINDCLRSAT 300

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Page 8

Db 181 FVPDCEDESKMKTSCVSSGSLMDPNITVETLDPQHLKRVDFLTWNESTPYOVLLESFSDS 240
QY 241 ENHSCFEHMHHPAPPEEFHORSNVTLLTNLKGCCRHVOVOIOPFFSSCLNDCLRHSAT 240
Db 241 ENHSCFEHMHHPAPPEEFHORSNVTLLTNLKGCCRHVOVOIOPFFSSCLNDCLRHSAT 300
QY 301 VSCPEMPDT--PEPIPDYPLM 320
Db 301 VSCPEMPDT--PEPIPDYPLM 320
QY 301 VSCPEMPDT--PEPIPDYPLM 320

RESULT 13
US-09-022-253-2
Sequence 2, Application US/09022253
Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
TELECOMMUNICATION NUMBER: 2617-B
TELEPHONE: (206)587-0430
TELEFAX: (206)587-0430
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-022-253-2

Query Match
Best Local Similarity 71.1%; Score 1254; DB 3; Length 864;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;
QY 1 MGAARSPVAVGPGILGLLLGLLAPGASRLLDHRAVYVSGDGLNCTVKNSTCDD 60
Db 1 MAIRKMPVAVGPGILGLLLGLLAPGASRLLDHRAVYVSGDGLNCTVKNSTCDD 60
QY 61 SWIHPRNLTSPSPDLQIQHFAHTQGDLPVAHENTLQTDASITYLEGAEISVQLN 120

Db 61 SWIHPRNLTSPSPDLQIQHFAHTQGDLPVAHENTLQTDASITYLEGAEISVQLN 120
QY 121 TNERLCVREFEPLSKLRHHRMRREFFSFVVDPOEYVTHLKPPIPDGDPHOSKNF 180
Db 121 TNERLCVREFEPLSKLRHHRMRREFFSFVVDPOEYVTHLKPPIPDGDPHOSKNF 180
QY 181 LVPDCEHARMKVTTPCKSSGSLMDPNITVETLEAQLNVSTLWNESTPYOVLLESFSDS 240
Db 181 LVPDCEHARMKVTTPCKSSGSLMDPNITVETLEAQLNVSTLWNESTPYOVLLESFSDS 240
QY 241 ENHSCFEHMHHPAPPEEFHORSNVTLLTNLKGCCRHVOVOIOPFFSSCLNDCLRHSAT 300
Db 241 ENHSCFEHMHHPAPPEEFHORSNVTLLTNLKGCCRHVOVOIOPFFSSCLNDCLRHSAT 300
QY 301 VSCPEMPDT--PEPIPDYPLM 320
Db 301 VSCPEMPDT--PEPIPDYPLM 320

RESULT 14
US-09-022-260-2
Sequence 2, Application US/09022260
Patent No. 6100235
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
TELECOMMUNICATION NUMBER: 2617-B
TELEPHONE: (206)587-0430
TELEFAX: (206)587-0430
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-022-260-2

Query Match
Best Local Similarity 71.1%; Score 1254; DB 3; Length 864;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

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	Index	Gaps
QY 1	MGARSPSSAVPGLGILLGLLVLPAGSARILDRALVCSQPLNCTYKNTCTLD	60
Db 1	mgarsspsavpaglglillllglvlapgastlrlldhnlavcsqplnctknsctldd	60
QY 61	SWIHRNLVSSPRDLQIOLFHFAHTQOGLFPAVHLEMTLQTDASTLYEGAEISVLQIN	60
Db 61	swihprnlvtssprkdlqldfhfchbqgqdlfrahlewllqdasillylegaelsvldn	120
QY 121	TNRLCVRFELSKLRHHRRRRRFFPSHNVDPDOEYEVYTHLHKPRPDGDPRHQSNNF	180
Db 121	tnerlcvrfeelsklrrhhrrrrrrffshnvdpdoeyevythlhpkrpdpdgdprhqsknf	180
QY 181	LYPDEHARAKTTLTCMSSGLMDPNIVELVEAHOLAVSTLWNSTHQTILTSPPHM	240
Db 181	lypdeharakttltcmssglmdpnivelvelaholavstlwnsthtqylltspfhm	240
QY 241	ENHSCFEHMHIPAPRPEFHQRSNVLTTLRNKGCGRHOVOIQPFSSCTLNCLHSAT	300
Db 241	enhscfehmhiaparpefhrqrsnvlltlnrkkgccrhovoiqpfssctlnclhsat	300
QY 301	VSCPEMDTPEPPIPDYMLW	320
Db 301	vscpepmdtpepripdymlw	320

	RESULT	2	
ID	AAW61272		
XX	AAW61272 standard; Protein; 866 AA.		
AC	AAW61272;		
DT	12-OCT-1998	(first entry)	
XX			
DE	Human interleukin-17 receptor.		
RW	Interleukin-17 receptor; IL-17 receptor; human; nitric oxide synthase; osteoarthritis; autoimmune disease; inflammation; therapy.		
KM			
XX			
OS	Homo sapiens.		
XX			
FH	Key:		
FT	Peptide	Location/Qualifiers	
FT		1..27	
FT	Protein	/label= Sig-peptide	
		28..866	

FT		/label= Mat_protein
FT	Protein	1..320
FT		/label= Soluble_II-17R
FT		/note= "Claim 2(b)"
FT	Domain	28..320
FT		/label= Extracellular
FT	Domain	31..341
FT		/label= Transmembrane
FT	Domain	342..866
FT		/label= Extracellular
FT		
PN	WO9823284-A1.	
PD	04-JUN-1998.	
PF	21-NOV-1997;	97WO-US21451.
PR	27-NOV-1996;	96US-0052525.
PA	(IMM) IMMUNEX CORP.	
PI	Troutt AB;	
DR	WIPI: 1998-332457/28.	
DR	N-PSDB; AA027552.	

Claim 2(b); Page 27-31; 41pp; English.

CC This polypeptide comprises human full-length interleukin-17
CC receptor (IL-17R). A claimed method for reducing the amount of
CC nitric oxide produced by a cartilage associated cell comprises
CC contacting the cell with a soluble IL-17R, especially claimed
CC soluble human or mouse (see AAM61271) IL-17R comprising the
CC peptide and extracellular domains of the respective full-length
CC receptors. Recombinant soluble IL-17R polypeptides can be obtained
CC using prokaryotic or eukaryotic (or glycosylated products)
CC expression systems. A cDNA sequence coding for full-length human
CC IL-17R is provided (see AAV27592). IL-17 is known to stimulate
CC nitric oxide production from cartilage-associated cells in
CC individuals with osteoarthritis. Inhibitors of nitric oxide
CC production, such as soluble IL-17R, may therefore be useful to
CC ameliorate the effects of nitric oxide in osteoarthritis as well as
CC in other disease conditions in which nitric oxide plays a role,
CC e.g. autoimmune and inflammatory diseases.
XX
XX Sequence 866 AA.

Query Match	100.08;	Score 1764;	DB 19;	Length 866;
Best Local Similarity	100.08;	Pred. No. 1.7e-169;		
Matches 320;	Conservative			

[illegible]

Tue Jul 17 11:27:35 2001

us-09-488-728-4_copy_1_320.rag

Db 241 enhscfemhnpaprippeefhgnsvltlrnlkgccrhqvqipffssclndclrhst 300
 OY 301 VSCPEMDTPEPTDYMPLW 320
 Db 301 vscpempdtpep1pdymp1w 320

RESULT 3
 AAW92409 standard; Protein: 866 AA.

AAW92409;
 21-APR-1999 (first entry)

Human IL-17R protein.

IL-17R; human; interleukin-17 receptor; immunoregulator; inhibitor;
 T cell proliferation; T cell activation; organ; graft; rejection;
 autoimmune disease; allergy; asthma; treatment; inflammatory disease;
 B cell proliferation; immunoglobulin secretion; immunogen.

Homo sapiens.

Key Location/Qualifiers
 Peptide 1..27
 /label= signal_peptide
 Protein 28..866
 /label= IL-17R

US5869286-A.

09-FEB-1999.

21-MAR-1996; 96US-0620694.

21-MAR-1996; 96US-0620694.

23-MAR-1995; 95US-0410535.

07-AUG-1995; 95US-0538765.

(IMMUNEX CORP.

Fanslow WC, Spriggs MK, Yao Z;

WPI; 1999-152766/13.

N-PSDB; AAX01922.

Isolated interleukin-17 receptor DNA - used to develop products for

treating e.g. organ or graft rejection, autoimmune disease, allergy,

asthma or inflammatory disease

Disclosure; Column 43-48; 25pp; English.

This sequence represents a human interleukin-17 receptor (IL-17R).
 IL-17R polypeptides have immunoregulatory activity. They can be used for
 inhibiting T cell proliferation, or for inhibiting T cell activation. In
 particular they can be used for preventing or treating organ or graft
 rejection, autoimmune disease, allergy or asthma. They can also be used
 for the prevention or treatment of inflammatory disease in which
 activated T cells play a role or for inhibiting B cell proliferation
 or immunoglobulin secretion. The IL-17 polypeptides can also be used
 as immunogens reagents in in vitro assays, or as binding agents for
 affinity purification procedures.

Sequence 866 AA;

Query Match 100.0%; Score 1764; DB 20; Length 866;
 Best Local Similarity 100.0%; Pred. No. 1,7e-169; Indels 0; Gaps 0;
 Matches 320; Conservative 0; Mismatches 0;

OY 1 MGAARSPFAVPGPLGLLLGLVAPGASLRLLDRALVCSQPLNCTVKNSTCLDD 60

Db 1 mgaarspsavpgpllglllllgvlapgaaslrllldhralvcsqplnctvknstcldd 60
 OY 61 SWIHRNLTSPSSPKDLOLQHPAHFOGDLFPVAHETWLOTQDASITYLEGASVTLQIN 120
 Db 61 swihprnltpsspkdlqlqhfahcggdlfpvahlewtclqdasllylegasv1qln 120
 OY 121 TNERLCVREFELSKLRHRRKRTFESHFVYDDQEVETVNHLPKPIPGDPHOSKNP 180
 Db 121 tnerlcvrfeflsklrhrtrwftishfvdpdqeyevtwhlpkpipgdphgsknf 180
 OY 121 tnerlcvrfeflsklrhrtrwftishfvdpdqeyevtwhlpkpipgdphgsknf 180
 Db 181 LVPOCEHARKKVTTPCMSGSLMDPNIVETLEAHQLRVSTLNSTHYQILLTSPPHM 240
 OY 181 lvpceharkkvttcpmsgslwdpnltveclleahqlrvstlnsthyqilltsp1hm 240
 Db 241 ENHSCFEMHHTIPAPRPEEFHORENSVTLTRNLKGCCRHQVOIOPEFSCINDCLRHSAV 300
 OY 241 enhscfemhhtipaprppeefhorensvltlrnlkgccrhqvqipffssclndclrhst 300
 Db 241 enhscfemhnpaprippeefhgnsvltlrnlkgccrhqvqipffssclndclrhst 300
 OY 301 VSCPEMDTPEPTDYMPLW 320
 Db 301 vscpempdtpep1pdymp1w 320

RESULT 4
 AAY99941 standard; Protein: 866 AA.

AAY99941;
 10-JAN-2001 (first entry)

Human IL-17R protein.

IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS 13;

murine; antibody; immune suppression.

Homo sapiens.

Key Location/Qualifiers
 Peptide 1..27
 /label= signal_peptide
 Domain 28..320
 /label= Extracellular_domain
 Domain 321..341
 /label= Transmembrane_domain
 Domain 342..866
 /label= Cytoplasmic_domain
 Protein 32..866
 /label= IL-17R

US6072037-A.

06-JUN-2000.

12-FEB-1998; 98US-0022696.

21-MAR-1996; 96US-0620694.

23-MAR-1995; 95US-0410535.

07-AUG-1995; 95US-0538765.

(IMMUNEX CORP.

Fanslow WC, Spriggs MK, Yao Z;

WPI; 2000-411206/35.

N-PSDB; AAG61240.

Antibodies immunoreactive with interleukin-17 receptor protein useful
 in interfering with receptor binding to CTLA-8, as components of the
 diagnostic or research assays or in affinity purification of the
 receptor -

PS Claim 1; Column 43-48; 25pp; English.

CC The present invention relates to a novel receptor that binds Interleukin
CC 17 (IL-17), also known as CTLA-8) and a Herpesvirus salmimiri homolog,
CC HVS13. The receptor is a type I transmembrane protein which is referred
CC to as IL-17R. Murine thymoma EL4 cells were found to express a
CC and a cDNA encoding the receptor was identified. The murine IL-17R cDNA
CC isolate DNA are described in AAA61238 and AAY99935. The cDNA was used to
CC present sequence is the human IL-17R protein. Soluble forms of the
CC receptor may be used to regulate immune responses, for example to
CC suppress rejection of organ grafts. Antibodies to IL-17R consisting of
CC amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be
CC useful as components of diagnostic or research assays. Such antibodies
CC may also be used in affinity purification of the receptor.

XX Sequence 866 AA:

Query Match Best Local Similarity 100.0%; Score 1764; DB 21; Length 866;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAARSPSAVPGPILGLLILGLVAPGASRLDHRALVCSOPGLNCTVNSCTCDD 60
DB 1 mgaarpspsavpgpiligllilglvapgastlrlldhravcsqpglncvksctcidd 60
QY 61 SWIHRNLTSPSPKDIOLHFHATQOGLFPAVHTEWTLQTDASILYEGAEISVQLN 120
DB 61 swihprnltpsspkdiolhfahatqogdlfpvahntewtlqtdasilyegaelsvqln 120
QY 121 TNERLCVREFEFLSKLRHNRKRFESHVNDPEYEVTHNLKRPIDGPNQSKNF 180
DB 121 tnerlcvrfeeflsklrhnrrkrfeshvndpeyevthnlkripdgpnqsknf 180
QY 181 LVPDCSHARKVYTPRCMSSGSLMDPNITVELTLEAHLRVSTLWNESTHYQILITSPFM 240
DB 181 lvpdcsharkvtprcmssgslmdpnitveltleahlrvtlwnesthyqilitsfpm 240
QY 241 ENHSCFEHMHIPARPEEFHONSNTLTLRNLKCCRRQVOYIOPEFSSCLNDCLRHSAT 300
DB 241 enhscfehmhiiparpeefhonsnvtltnrlkccrrqvoiopefssclndclrhhsat 300
QY 301 VSCPEMDTPPEPIPDYMWPLW 320
DB 301 vscpempdtpepidpymplw 320

RESULT 5

AA97131
ID AAY97131 standard; Protein; 866 AA.

AC AAY97131;
DT 04-DEC-2000 (first entry)

DE Human interleukin-17 receptor.

KW IL-17R, interleukin-17 receptor; soluble; CTLA-8; Herpesvirus salmimiri;
KW HVS13; graft rejection; suppressor; immunosuppressive; anti-allergic;
XX anti-asthmatic.

OS Homo sapiens.

XX Key
XX Peptide Location/Qualifiers
XX 1..27

FT Protein /label= Signal_peptide
FT 28..866

FT Protein /label= Mature_protein
FT 1..320

FT Domain /label= Soluble_IL-17_receptor
FT 28..320

FT Domain /label= Extracellular_domain
FT 321..341
FT Domain /label= Transmembrane_domain
FT 342..866
FT /label= Cytoplasmic_tail

US6100235-A.

08-AUG-2000.

11-FEB-1998; 98US-0022260.

21-MAR-1996; 96US-0620694.

23-MAR-1995; 95US-0410535.

07-AUG-1995; 95US-0538765.

(IMM) IMMUNEX CORP.

Fanslow WC, Spriggs MK, Yao Z;
WPI: 2000-548298/50.

N-PSDB: AAA51988.

Regulating, treating or preventing immune or inflammatory response in a
mammal, especially organ or graft rejection, allergy or asthma,
comprises administering interleukin-17 receptors

Claim 1; Column 43-48; 26pp; English.

A novel interleukin-17 receptor (IL-17R) was identified by screening a
cDNA library from T cell thymoma EL4 cells, which were identified as
binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
region and soluble IL-17 (CTLA-8) protein or a homologous
Herpesvirus salmimiri (HVS) protein, designated HVS13. Regulating an
immune or inflammatory response in a mammal comprises administering
soluble IL-17R. Residues 1-320 of the human IL-17R, and fragments of
extracellular domain that bind IL-17. The method is useful for regulating
an immuneresponse, for treating or preventing diseases like allergy,
asthma and autoimmune diseases, and for suppressing rejection of grafted
organs or tissues in the recipient.

Sequence 866 AA:

Query Match Best Local Similarity 100.0%; Score 1764; DB 21; Length 866;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAARSPSAVPGPILGLLILGLVAPGASRLDHRALVCSOPGLNCTVNSCTCDD 60
DB 1 mgaarpspsavpgpiligllilglvapgastlrlldhravcsqpglncvksctcidd 60
QY 61 SWIHRNLTSPSPKDIOLHFHATQOGLFPAVHTEWTLQTDASILYEGAEISVQLN 120
DB 61 swihprnltpsspkdiolhfahatqogdlfpvahntewtlqtdasilyegaelsvqln 120
QY 121 TNERLCVREFEFLSKLRHNRKRFESHVNDPEYEVTHNLKRPIDGPNQSKNF 180
DB 121 tnerlcvrfeeflsklrhnrrkrfeshvndpeyevthnlkripdgpnqsknf 180
QY 181 LVPDCSHARKVYTPRCMSSGSLMDPNITVELTLEAHLRVSTLWNESTHYQILITSPFM 240
DB 181 lvpdcsharkvtprcmssgslmdpnitveltleahlrvtlwnesthyqilitsfpm 240
QY 241 ENHSCFEHMHIPARPEEFHONSNTLTLRNLKCCRRQVOYIOPEFSSCLNDCLRHSAT 300
DB 241 enhscfehmhiiparpeefhonsnvtltnrlkccrrqvoiopefssclndclrhhsat 300
QY 301 VSCPEMDTPPEPIPDYMWPLW 320
DB 301 vscpempdtpepidpymplw 320

Query Match	100.0%;	Score 1764;	DB 21;	Length 866;
Best Local Similarity	100.0%;	Pred. No. 1.7e-169;	Mismatches 0;	Indels 0;
Matches 320;	Conservative	0;	Indels	Gaps
OY	1	MGARSPSPSAVPGPLGLALLLLGLVLAAGASRLDHRALVCSOPGLNCTVKNSTCDD	60	
Db	1	mgarspspsavpgpllglllllgvldaggasrlldhralvcsqplnctvknstcdd	60	
OY	61	SWIHPRNLTSPSSPMDLIQLHFAHQCGLDFPVNHTIEMTLQTDASTIYLGAELSVQLN	120	
Db	61	swihprnltpsspmdliqlhfhantqgdlfrvahlewlqltqdasillylegaelsvqln	120	
OY	121	TNERLCVRFPEELSKRHHRRMRWFESHFVVDPODEXEVTVNHLKPRIPDGDPRHOSKNF	180	
Db	121	tnerlcvtvfeflsklrhhrrmrwfeshfvdppdgyevtvnhlpkripdgdprhgsknf	180	
OY	181	LYPDCEHARMKYTPQCMSSGLMDPNITVETLEAHOLVSPFLMNESTHYQILITSPFHM	240	
Db	181	lypdceharmkvtlpcmssgslwdpnltvclleaqlvstflmnesthqylltsfphm	240	
OY	241	ENHSGEPHMHHTPARPEEFHORSNTLTLRNLKGCRRHOVOIOFPFSSCLMDCLRHSAT	300	
Db	241	enhsclehmhhpapeefhgrsntltlrnlkgccrhqvqipffssclndclrhset	300	
OY	301	VSCPEMPDPPEPIPDYMLTW	320	
Db	301	vscpempdppepidymplw	320	
RESULT	7			
ID	AAB03807	standard; Protein: 866 AA.		
AC	AAB03807;			
DT	13-OCT-2000	(first entry)		
DE	Human Interleukin-17 (IL-17) receptor protein sequence.			
KW	Interleukin-17 receptor; IL-17R; CTLA8; antiinflammatory; anti allergic;			
KW	immunosuppressive; organ rejection; graft rejection; autoimmune disease;			
KW	allergy; asthma; human.			
OS	Homo sapiens.			
XX	US6072033-A.			
XX	06-JUN-2000.			
XX	11-FEB-1998;	9805-0022255.		
XX	21-MAR-1996;	9605-0620694.		
XX	23-MAR-1995;	9505-0410535.		
XX	07-AUG-1995;	9505-0538765.		
XX	(IMMUNEX CORP.			
XX	Fanslow WC, Spriggs MK, Yao Z;			
XX	WPI: 2000-411205/35.			
XX	N-PESDB; AAA59871.			
XX	Interleukin-17 receptor protein useful for regulating immune functions			
XX	and for preventing or treating organ or graft rejection, autoimmune			
XX	disease, allergy or asthma in human			
XX	Claim 1; Column 43-48; 26pp; English.			
XX	This invention relates to an isolated and purified interleukin-17			
XX	receptor (IL-17R). A soluble IL-17 protein (CTLA8) and a herpesvirus			
XX	stamiri (HVS13) open reading frame (homologous to CTLA8) were expressed			
XX	as fusion proteins comprising an immunoglobulin Fc region, and used to			

CC screen for the expression of the IL-17R. The screening identified the
 CC novel receptor of the invention. IL-17R is a type I transmembrane
 CC protein that exhibits antiinflammatory, immunosuppressive, antiasthmatic
 CC and anti-allergic activities, and is an inhibitor of T cell proliferation
 CC and activation. IL-17R can be used to regulate immune functions, and is
 CC useful for preventing or treating organ or graft rejection, autoimmune
 CC disease, allergy or asthma. The present sequence represents the human
 CC interleukin-17 receptor amino acid sequence identified in the invention.
 SQ Sequence 866 AA;

Query Match 100.0%; Score 1764; DB 21; Length 866;
 Best Local Similarity 100.0%; Pred. No. 1.7e-169;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAARSPSAVPGPLGLLLGLLGLVLAAPGASLRDLDRALVCSQGLNCTVKNSTCLDD 60
 DB 1 mgaarpspsavpgpllgllllglvlapggsalrldhralvcsqglinctvknstcldd 60
 QY 61 SWIHPRLTPSSPKDLOQLHFAHTOOGDLFPVAHTEMTLOTDASTILEGALSVLOLN 120
 DB 61 swihprnltpsspkdlqlghlfahtqgdlfpvahlewltqdasillyegalsvlgln 120
 QY 121 TNRRLCVREFLSKLRRHRRMRTFSHPVDPDQEVTVVHLLKRPIDGDPNHSKNF 180
 DB 121 tnrllcvreflsklrrhrrmrtfshpvdppdqeyvtvnhllkripdgdpmhsknf 180
 QY 181 LVPDCEHARKVTPPCMSGSLMDPNITVELEAHLRVSTLWNESTHYOILLTSPFHM 240
 DB 181 lvpdceharmkvtppcmsgslwdpnlveteleahqrvstlwnesthyltllstfphm 240
 QY 241 ENHSCFEHMHHPAPPEFHORSNVTLLRNKGCCHQVOIQPFSSCINDCLRISAT 300
 DB 241 enhscfehmhhpaprpeefhorskvnvtllrnkgccchqvoioqpfsscindclrnsat 300
 QY 301 VSCPEMPPTPEPIDYMLW 320
 DB 301 vscpempptpepidymplw 320

RESULT 8

AAB62066
 ID AAB62066 standard; Protein; 866 AA.
 XX AAB62066;

XX 29-MAY-2001 (first entry)

DE Human IL-17R (hCTLA-8 receptor) polypeptide.

KW CTLA-8; interleukin-17; IL-17; IL-17 receptor; IL-17R; human;
 XX immunosuppressive; anti-allergic; antiasthmatic; antiinflammatory.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..27
 FT Protein /note= "signal peptide"
 FT Protein 28..866

FT Domain /note= "mature protein"
 FT Domain 28..320

FT Domain /note= "extracellular domain"
 FT Domain 321..341

FT Domain /note= "transmembrane domain"
 FT Domain 342..866

XX Domain /note= "cytoplasmic domain"

US6197525-B1.
 06-MAR-2001.
 11-FEB-1998; 98US-0022257.

XX 21-MAR-1996; 96US-0620694.
 PR 23-MAR-1995; 95US-0410535.
 PR 07-AUG-1995; 95US-0538765.
 XX (IMV) IMMUNEX CORP.

PI Yao Z, Spriggs MK, Fanslow WC;

DR WPI: 2001-234480/24.
 DR N-PSDB: AAF57188.

PT New assay kits for detecting interleukin-17 (IL-17), IL-17 receptors
 PT and (antagonists or mimetics of) the interaction between IL-17 and
 PT IL-17 receptor, useful for treating autoimmune diseases -
 PS Claim 1; Columns 37-44; 26pp; English.

CC The invention is directed towards assays for detection of interleukin-17
 CC (IL-17), IL-17 receptor (IL-17R), and (antagonists or mimetics of) the
 CC interaction between IL-17 and IL-17R. The assay kit comprises an IL-17R
 CC protein and a detecting reagent. The method is useful for inhibiting
 CC binding of IL-17 to cells expressing IL-17R. IL-17 receptors are also
 CC useful for preventing or treating organ or graft rejection, autoimmune
 CC diseases, allergy, asthma and inflammatory diseases in which activated
 CC T-cells play an important role. The present sequence represents a
 CC human IL-17R (hCTLA-8 receptor) polypeptide.
 SQ Sequence 866 AA;

Query Match 100.0%; Score 1764; DB 22; Length 866;
 Best Local Similarity 100.0%; Pred. No. 1.7e-169;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAARSPSAVPGPLGLLLGLLGLVLAAPGASLRDLDRALVCSQGLNCTVKNSTCLDD 60
 DB 1 mgaarpspsavpgpllgllllglvlapggsalrldhralvcsqglinctvknstcldd 60
 QY 61 SWIHPRLTPSSPKDLOQLHFAHTOOGDLFPVAHTEMTLOTDASTILEGALSVLOLN 120
 DB 61 swihprnltpsspkdlqlghlfahtqgdlfpvahlewltqdasillyegalsvlgln 120
 QY 121 TNRRLCVREFLSKLRRHRRMRTFSHPVDPDQEVTVVHLLKRPIDGDPNHSKNF 180
 DB 121 tnrllcvreflsklrrhrrmrtfshpvdppdqeyvtvnhllkripdgdpmhsknf 180
 QY 181 LVPDCEHARKVTPPCMSGSLMDPNITVELEAHLRVSTLWNESTHYOILLTSPFHM 240
 DB 181 lvpdceharmkvtppcmsgslwdpnlveteleahqrvstlwnesthyltllstfphm 240
 QY 241 ENHSCFEHMHHPAPPEFHORSNVTLLRNKGCCHQVOIQPFSSCINDCLRISAT 300
 DB 241 enhscfehmhhpaprpeefhorskvnvtllrnkgccchqvoioqpfsscindclrnsat 300
 QY 301 VSCPEMPPTPEPIDYMLW 320
 DB 301 vscpempptpepidymplw 320

RESULT 9

AAV72754
 ID AAV72754 standard; Protein; 866 AA.
 XX AAV72754;

XX 31-MAY-2001 (first entry)

DE Human Interleukin-17 receptor (IL-17R) or CTLA-8 receptor.

KW Human; Interleukin-17 receptor; IL-17R; immunosuppressive; anti-allergic;
 KW antiasthmatic; antiinflammatory; graft rejection; autoimmune disease;
 KW inflammatory disease; allergy; CTLA-8; immunogen; asthma.

XX
OS Homo sapiens.

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1::2/  
/label= signal_peptide
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28..866 Mature human IL-17_receptor

28..320

321..341

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label = 'Transilvania-2'
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/label= cytoplasmic_tall
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[illegible]

96US-0620694.
96US-0410535

95US-0538765.

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901/22.
315.

of grafted organ

mastering to recipient a

/ Receiver Process-

mm 43-48; 26pp; English.

sequence is human Interleu-

library by cross-species

relates to intelligence

membrane protein which

in a graft recipient.

or preventing or treating asthma,

cells play a role. Soluble

For the experiments described as immunogens, reagents

Infinity Purification Process

166 AA;

100.0%;	score
100.0%;	Pred: 1

Conservative	0;	Mismanagement
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PPSAVPGPIGLLLGLVLA PGGA

[illegible]

PROSTATE

NTLTPSPFDDVIXE

anltprspkd1q1qlnranlq99u

SVRFEELSKLRHHRRWRETFSHEV

urfe]sklrhhrrwrtfshfv

.....WDPNITIVE

100

CC an immunoresponse for suppressing rejection of grafted organs or tissues
CC in the recipient and for treating or preventing diseases like allergy,
CC asthma and autoimmune diseases.
CC Note: This sequence does not appear in the specification. It was created
CC from the full length murine IL-17R (see AAY97180) and the flag peptide
CC (see AAY97183)
xx
SQ Sequence 330 AA:

Query Match	71.1%	Score 1254	DB 21	Length 330
Best Local Similarity	71.4%	Pred. No. 1.7e-118		
Matches 230	Conservative 30	Mismatches 60	Indels 2	Gaps 1
QY	1	MGAAKSPSPAA	RGRLGILLILLGLVLR	GGASLRLLDNRALVSGPGLNYKNSCLSD
Db	1	maitrcewryv	rgpalslgwlllllllnv	laprasprllldfarpvcaqeglsctvksntclld
QY	61	SWINRNLVTSSP	DDIOLOIHF	FAHTFOOGDFEPAVNIEMTLQTDASTLYLEGAELSVLOLN
Db	61	swlnrknlrps	spknljnlsvs	stghelrvprlllnwewtlrldctaslllydegelsvldln
QY	121	TNRRLCRFEFL	KLKLNHRKRRKFR	SHFNVVDRODEYTVNHLKRPRLRDPDPMHOSKNF
Db	121	tnerlcwkgf	lsmldqhlkwt	rfsfshlvvdprgseylevthhlpkrpddgdpnhkskii
QY	181	LYRDESHAKMKV	TLTROMSGSLMDN	INVELLEAHOLVNSTLIMNESTHVIQILTSPRHM
Db	181	lyrdeedskmk	tktsccvsgslwpr	llveclldqhlrvdfclwnestpvyvllsestds
QY	241	ENHSCEFHNNH	NRARREEPNORSN	VTLLTNLKGCRHOVIOOPRSSCLNDCLRHSAAT
Db	241	enhsctdv	vkqdlfbrpgeef	ngqranvftlskfwscshhqvqpfisscldncilrhavt
QY	301	VSCRMMDT--	PEETPRYPLM	320
Db	301	vscrvsnltv	krpvadyldlw	322

AA97258	RESULT 11
ID	AA97258 standard; peptide; 330 AA.
XX	
AC	AA97258;
XX	
DT	04-DEC-2000 (first entry)
XX	
DE	Soluble IL-17R/Flag fusion protein.
XX	
KW	IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri
KW	HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KM	anti-asthmatic; flag epitope; fusion protein.
OS	Mus sp.
XX	
FH	Key
FT	Protein
FT	Peptide
FT	Peptide
FT	Protein
FT	Peptide
FN	US6100235-A.
PD	08-AUG-2000.
XX	
PF	11-FEB-1998;
XX	
PR	21-MAR-1996;
PR	23-MAR-1995;
	96US-0620694.
	95US-0410535.
	98US-0022260.
	/label= Soluble_IL-17_receptor
	1..31
	/label= Signal_peptide
	32..322
	/label= IL-17_receptor_extracellular_domain
	323..330
	/label= Flag_epitope

XX	07-AUG-1995;	95US-0538765.
PR		
XX		
PA	(IMMV) IMMUNEX CORP.	
XX		
XX	Fanslow MC, Springs MK, Yao Z;	
PI		
XX	WPI; 2000-548298/50.	
DR		
XX		
PT	Regulating, treating or preventing immune or inflammatory response in a	
PT	mammal, especially organ or graft rejection, allergy or asthma,	
PT	comprises administering interleukin-17 receptors	
PS		
XX	Example 3; Column -; 27pp; English.	
XX		
CC	A novel interleukin-17 receptor (IL-17R) was identified by screening a	
CC	cDNA library from T cell thymoma EL4 cells, which were identified as	
CC	binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc	
CC	region and soluble IL-17 (CTLA-8) protein or a homologous	
CC	Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an	
CC	immune or inflammatory response in a mammal comprises administering	
CC	soluble IL-17R. Soluble IL-17R fragments comprise residues 1-322 of the	
CC	murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the	
CC	extracellular domain that bind IL-17. The method is useful for	
CC	regulating an immunoresponse, for treating or preventing diseases like	
CC	allergy, asthma and autoimmune diseases, and for suppressing rejection of	
CC	grafted organs or tissues in the recipient.	
CC	Note: This sequence does not appear in the specification. It was created	
CC	from the full length murine IL-17R (see AAY97130) and the flag peptide	
CC	(see AAY97132)	
XX		
XX		
Sequence	330 AA:	

Query Match	Best Local Similarity	71.1%;	Score 1254;	DB 21;	Length 330;
Matches 230;	Conservative 30;	Mismatches 60;	Indels 2;	Gaps 1	
QY 1	MGARSPPSAVDPRLGLLLLLGLVLRGASLRLLDHRALVCSQPLNCTVKNSTCLDD	60			
Db 1	matrlcwprvvpqpalgwlllllnvlapysaprlldfpavcagqelscrvnksncldd	60			
QY 61	SWHPENLTPESSPKDLQQLHFHTQGDLEFPVNIEMTLQTDASTLTLLEGALSTYLDLN	60			
Db 61	swlhpknltpspknlhlnlsvsstqgelvprvlhwewllqtaslllylegaelvlgln	120			
QY 121	TNERLCVAFPEELSKLRHHNRMRFTFSHFVDDDOCVETVYNNHLEKPRIPDGDPNQSKNF	180			
Db 121	tnerlcsvqfqlsmqlphkrktrfshfshfvdpqgeyevtlhpkripdgdgnhkskll	180			
QY 181	LVPDCEHARMKVVTTPCQSSGLMDPNIVETLEAQLRVSFILMNESHYQDILTLSPPHM	240			
Db 181	fvpdcedskmkmtscsvsagslwdpnlvteltdtghlrvfdflwnestpryvllestfsds	240			
QY 241	ENHSCFHHNHILPARPEEFHQRNSNTLLRLRLKSCCHQVOIQPFSSCLINDCLRHSAT	300			
Db 241	enhscldvkvkqflfarpqeehfgdranvftlskfncwhcnhqvqpfissclndclrhavt	300			
QY 301	VSCPENPDT--PEPIPDYKPLW 320				
Db 301	vpcvsnltvtpkpvadyldplw 322				
RESULT 12					
AAW04184					
ID	AAW04184 standard; Protein; 864 AA.				
AC	AAW04184;				
XX					
XX					
DT	05-DEC-1996 (first entry)				
XX					
DE	Murine Interleukin-17 receptor.				
XX					
KW	Interleukin-17 receptor; IL-17R; autoimmune disease; allergy;				

Tue Jul 17 11:27:35 2001

us-09-488-728-4_copy_1_320.rag

KW asthma; graft rejection; inflammation; cytokine; therapy.

XX Mus sp.

OS Location/Qualifiers

PH Key

FT 1..31

FT /label= Sig-peptide

FT 32..322

FT /label= Extracellular_domain

FT 323..343

FT /label= Transmembrane_domain

FT 344..864

FT /label= Cytoplasmic_tail

XX Domain

XX WO9629408-A1.

XX 26-SEP-1996.

XX 21-MAR-1996; 96WO-US04018.

XX 07-AUG-1995; 95US-0538765.

XX 23-MAR-1995; 95US-0410535.

XX (IMMUNEX CORP.

XX Fanslow WC, Spriggs MK, Yao Z;

XX WPI: 1996-443184/44.

XX N-PSDB: AAT33800.

XX DNA encoding interleukin-17 receptor - useful for regulating immune and inflammatory responses, or to suppress graft rejection

XX Claim 1: Page 29-32; 52pp; English.

XX The murine interleukin-17 receptor (IL-17R) (AAW04184) is a type I transmembrane protein that binds IL-17 (CTLA-8, see also AAW02386) and HVSI3 (AAW02387), a viral homologue of IL-17. Its amino acid sequence was deduced from a cDNA clone (AAT33800) isolated from murine thymoma EL4 cells. Soluble, recombinant forms of the receptor (partic. amino acids 1-322) can be prep'd. in transformed host cells and used to regulate immune and inflammatory responses, in methods for suppressing rejection of grafted organs or tissue, and in assays of IL-17 and IL-17R.

XX Sequence 864 AA:

XX Query Match 71.1%; Score 1254; DB 17; Length 864;

XX Best Local Similarity 71.4%; Pred. No. 6.7e-118;

XX Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

QY 1 MGAARSPSAVPGILGLLLLLGLVAPGASLRLLDRAVCSOPGINCTVKNSTCLDD 60

DB 1 mairtceprvppalgwlllllnvlaprasprllidfpaycaeglsctrvkstcld 60

QY 61 SWIHPNLTSSSKDQIOLFHATQOGLFVNAHLEWTLTQDASTLYLEGAELSVLDLN 120

DB 61 swlhpnltspskdniofahatqoglfvnahlewtltqdstlylegealsvldln 120

QY 61 swlhpnltspskdniofahatqoglfvnahlewtltqdstlylegealsvldln 120

DB 61 swlhpnltspskdniofahatqoglfvnahlewtltqdstlylegealsvldln 120

QY 121 TNERLCYFEFLSKLRHHRMRFTFSHFVVDDEEVVNHLPRTIDGDPNHOQKMF 180

DB 121 tnerlcyfelfsklrhhrmrftfshfvvddeevvnhlprtidgdpnhoqkmf 180

QY 121 tnerlcyfelfsklrhhrmrftfshfvvddeevvnhlprtidgdpnhoqkmf 180

DB 121 tnerlcyfelfsklrhhrmrftfshfvvddeevvnhlprtidgdpnhoqkmf 180

QY 181 LVPPDEAHKMTVTPCMSSGLAMPNITVETLEAHQLRVSTFMNENSTVOIILTFPHM 240

DB 181 lvppdeahkmtvtpcmssglampnitvetleahqlrvstfmnenstvoilftphm 240

QY 181 lvppdeahkmtvtpcmssglampnitvetleahqlrvstfmnenstvoilftphm 240

DB 181 lvppdeahkmtvtpcmssglampnitvetleahqlrvstfmnenstvoilftphm 240

QY 241 ENHSCFEHMHNIAPRPEFHORSNVTILRNKGCCHQVOIQPFSSCLNDCIRHSAT 300

DB 241 enhscfehmhniaprpefhorstnvtilrnkgcchqvoiqpfssclndcirsat 300

QY 241 enhscfehmhniaprpefhorstnvtilrnkgcchqvoiqpfssclndcirsat 300

DB 241 enhscfehmhniaprpefhorstnvtilrnkgcchqvoiqpfssclndcirsat 300

QY 301 VSCPEMPDT-PEPIPDYMLW 320

DB 301 vscpempdtvpkpvadyiplw 322

RESULT 13

AAW61271

ID AAW61271 standard; Protein; 864 AA.

AC AAW61271;

XX 12-OCT-1998 (first entry)

XX Mouse interleukin-17 receptor.

XX Interleukin-17 receptor; IL-17 receptor; mouse; nitric oxide; cartilage; osteoarthritis; autoimmune disease; inflammation; therapy.

XX Mus sp.

XX Location/Qualifiers

XX Key

XX 1..31

XX /label= Sig-peptide

XX 32..864

XX /label= Mat_protein

XX Protein

XX 1..322

XX /label= Soluble_IL-17R

XX /note= "Claim 2(a)"

XX 32..322

XX /label= Extracellular

XX 323..343

XX /label= Transmembrane

XX 344..864

XX /label= Extracellular

XX Domain

XX WO9823284-A1.

XX 04-JUN-1998.

XX 21-NOV-1997; 97WO-US21451.

XX 27-NOV-1996; 96US-0052525.

XX (IMMUNEX CORP.

XX Troutt AB;

XX WPI: 1998-322457/28.

XX N-PSDB: AAV27591.

XX Reducing nitric oxide production by cartilage associated cells - by contacting cells with soluble interleukin-17 receptor, useful to treat osteoarthritis and autoimmune and inflammatory diseases

XX Claim 2(a): Page 20-23; 41pp; English.

XX This polypeptide comprises mouse full-length interleukin-17 receptor (IL-17R). A claimed method for reducing the amount of nitric oxide produced by a cartilage associated cell comprises contacting the cell with a soluble IL-17R, especially claimed soluble murine or human (see AAW61272) IL-17R comprising the signal peptide and extracellular domains of the respective full-length receptors. Recombinant soluble IL-17R polypeptides can be obtained using prokaryotic or eukaryotic (for glycosylated products) expression systems. A cDNA sequence (see AAV27591) coding for full-length murine IL-17R is provided. IL-17 is known to stimulate nitric oxide production from cartilage-associated cells in individuals with osteoarthritis. Inhibitors of nitric oxide production, such as soluble IL-17R, may therefore be useful to ameliorate the effects of nitric oxide in osteoarthritis as well as in other disease conditions in which nitric oxide plays a role, e.g. autoimmune and inflammatory diseases.

SQ Sequence 864 AA;

Query Match
Best Local Similarity 71.4%; Score 1254; DB 19; Length 864;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

QY 1 MGARSPSAVPGPLGLLLGLVAPGASLRLLDHRALVCSOPGLNCTVKNSTCLDD 60
DB 1 mairtcwprvvpapalqwlilllnvlaprasprllldfpavcageglscrvkstcldd 60
QY 61 SWIHRNLTSSRKDLQIOIHFANTOQDLFPVAHLEWTLQTDASITLLEGAEISVLQLN 120
DB 61 swihprnltpssrkdlqioihfantoqdlfpvahnlewtlqtdasitllegaelsvlqln 120
QY 121 TNERLCVREFEFLSKLRHHRMRFTSHFVNDPDEYVTVVHNLKPKIPDDDPNHQKNF 180
DB 121 tnerlcvkrefeelsklrhhrrmrftshfvndpdeyvtvvhnlkpkipdddpnhqknf 180
QY 181 LVPDCEHARMKVTPCMSSGSLMDPNITVEFLNAHOLRVSEFTLNVESTHYOILLTSPPH 240
DB 181 lvpdcsharmkvtpcmssgslmdpnitveflnaholrvseftlnvesthyoilltspph 240
QY 241 ENHSCFEHMHIIIPARPEEFHQRNSVTLTLNLKGCCHQVOYOQPFSSCLNDCLRHSAT 300
DB 241 enhscfdvvhkqilaprgqefhqransvltltnlkgccrhqvoyoqpfssclndclrhSAT 300
QY 301 VSCPEMPDT--PEPIPDYMPLM 320
DB 301 vpcpvlsnttvpkpvadyiplw 322

RESULT 14

AAW92408
ID AAW92408 standard; Protein; 864 AA.

AAW92408;

21-APR-1999 (first entry)

Murine IL-17R protein.

IL-17R; murine; interleukin-17 receptor; immunoregulator; inhibitor;
T cell proliferation; T cell activation; organ; graft; rejection;
autoimmune disease; allergy; asthma; treatment; inflammatory disease;
B cell proliferation; immunoglobulin secretion; immunogen.

Mus sp.

Key Location/Qualifiers

FT Peptide 1..31

FT Protein /label= signal_peptide 32..864

US5869286-A.

09-FEB-1999.

21-MAR-1996; 96US-0620694.

21-MAR-1996; 96US-0620694.

23-MAR-1995; 95US-0410535.

07-AUG-1995; 95US-0538765.

(IMAV) IMMUNEX CORP.

Fanslow WC, Spriggs MK, Yao Z;

WPI; 1999-152766/13.

N-PSDB; AAX01921.

Isolated interleukin-17 receptor DNA - used to develop products for
treating e.g. organ or graft rejection, autoimmune disease, allergy,

PT asthma or inflammatory disease
XX Disclosure; Column 25-30; 25pp; English.

This sequence represents a murine interleukin-17 receptor (IL-17R).
IL-17R polypeptides have immunoregulatory activity. They can be used for
inhibiting T cell proliferation, or for inhibiting T cell activation. In
particular they can be used for preventing or treating organ or graft
rejection, autoimmune disease, allergy or asthma. They can also be used
for the prevention or treatment of inflammatory disease in which
activated T cells play a role or for inhibiting B cell proliferation
or immunoglobulin secretion. The IL-17 polypeptides can also be used
as immunogens, reagents in in vitro assays, or as binding agents for
affinity purification procedures.

SQ Sequence 864 AA;

Query Match
Best Local Similarity 71.4%; Score 1254; DB 20; Length 864;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

QY 1 MGARSPSAVPGPLGLLLGLVAPGASLRLLDHRALVCSOPGLNCTVKNSTCLDD 60
DB 1 mairtcwprvvpapalqwlilllnvlaprasprllldfpavcageglscrvkstcldd 60
QY 61 SWIHRNLTSSRKDLQIOIHFANTOQDLFPVAHLEWTLQTDASITLLEGAEISVLQLN 120
DB 61 swihprnltpssrkdlqioihfantoqdlfpvahnlewtlqtdasitllegaelsvlqln 120
QY 121 TNERLCVREFEFLSKLRHHRMRFTSHFVNDPDEYVTVVHNLKPKIPDDDPNHQKNF 180
DB 121 tnerlcvkrefeelsklrhhrrmrftshfvndpdeyvtvvhnlkpkipdddpnhqknf 180
QY 181 LVPDCEHARMKVTPCMSSGSLMDPNITVEFLNAHOLRVSEFTLNVESTHYOILLTSPPH 240
DB 181 lvpdcsharmkvtpcmssgslmdpnitveflnaholrvseftlnvesthyoilltspph 240
QY 241 ENHSCFEHMHIIIPARPEEFHQRNSVTLTLNLKGCCHQVOYOQPFSSCLNDCLRHSAT 300
DB 241 enhscfdvvhkqilaprgqefhqransvltltnlkgccrhqvoyoqpfssclndclrhSAT 300
QY 301 VSCPEMPDT--PEPIPDYMPLM 320
DB 301 vpcpvlsnttvpkpvadyiplw 322

RESULT 15

AAW99935 standard; Protein; 864 AA.

AAW99935;

10-JAN-2001 (first entry)

Murine IL-17R protein.

IL-17R; murine; interleukin 17; Herpesvirus salmanti; HVS 13;

murine; antibody; immune suppression.

Mus sp.

Key Location/Qualifiers

FT Peptide 1..31

FT Domain /label= signal_peptide 32..322

FT Domain /label= Extracellular_domain 323..353

FT Domain /label= Transmembrane_domain 354..864

FT Domain /label= Cytoplasmic_domain 32..864

FT Protein /label= IL-17R

Search completed: July 17, 2001, 11:18:55
 Job time: 194 sec

XX US6072037-A.
 PN 06-JUN-2000.
 PD 12-FEB-1998; 98US-0022696.
 XX
 PF 21-MAR-1996; 96US-0620694.
 PR 23-MAR-1995; 95US-0410535.
 PR 07-AUG-1995; 95US-0538765.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Fanslow WC, Spriggs MK, Yao Z;
 XX WPI: 2000-411206/35.
 DR N-PSDB; AAA61238.
 XX

Antibodies immunoreactive with interleukin-17 receptor protein useful in interfering with receptor binding to CTLA-8, as components of diagnostic or research assays or in affinity purification of the receptor -

Claim 1; Column 25-30; 25pp; English.

The present invention relates to a novel receptor that binds interleukin 17 (IL-17, also known as CTLA-8) and a Herpesvirus salmuri homolog, HVS13. The receptor is a type I transmembrane protein which is referred to as IL-17R. Murine thymoma EL4 cells were found to express a receptor for IL-17. An EL4 mammalian expression library was screened and a cDNA encoding the receptor was identified. The present sequence is the murine IL-17R protein. The cDNA was used to isolate DNA encoding human IL-17R by cross species hybridisation. The human IL-17R cDNA and protein are described in AAA61240 and AAY9941. Soluble forms of the receptor may be used to regulate immune responses, for example to suppress rejection of organ grafts. Antibodies to IL-17R consisting of amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be useful as components of diagnostic or research assays. Such antibodies may also be used in affinity purification of the receptor.

Sequence 864 AA;

Query Match 71.1%; Score 1254; DB 21; Length 864;
 Best Local Similarity 71.4%; Pred. No. 6,7e-118;
 Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

QY 1 MGAARSPSAVAGPLGLGLLLGLVLAAPGASLRLLDHRALVCSQPGLNCTYKNSCTCDD 60
 DB 1 mairrcwprvvpypgalgwlllllnvlapgrasprlldfpaycageglscrvknstcldd 60
 QY 61 SWIHRNLTSPSSPKDLQLOLFAHMQGDLFPVAHIEWTLOTDAITLYEGAEISVLQIN 120
 DB 61 swihpknltpsspkdlylnlsvstclqgelvplvhwelclqdasillyeaealsvqln 120
 QY 121 TNERLCVREFEYSKLRHHRWRFTFSHFVVDPEYEVTVHHLPRIPDGFPHQSKNF 180
 DB 121 tnerlcwkrqfismqlghkkrwfshtvvdpggeyevtvhlprkpdgdnkskii 180
 QY 181 LVPDCHEARKYVTPCMSSGLMDPNIVETLEFAHOLRVSTLWNESTHQLLTSEPHM 240
 DB 181 lvpdccksmkmtscvssglwvdpnlvctldqhlrvdfllwnestlpyqvllesfsds 240
 QY 241 ENHSCFEHNNHITAPRPEEHORSNTLTLRNKGCRCRHOVOIOPEFSSCLINDCLRHSA 300
 DB 241 enhscfdvkvqifaprqeefthgravvftlskthwcnhivqvqffissclndclrhavt 300
 QY 301 VSCPEMPDT--PERIPDYMPLW 320
 DB 301 vpcpvisntlvcpkvadylplw 322

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 17, 2001, 11:18:01 ; Search time 38:21 Seconds
(without alignments)
1114.949 Million cell updates/sec

Title: US-09-488-728-2_COPY_1_322
Perfect score: 1766
Sequence: 1 MAIRRCMPRVVPGALGWL.....CPVISNTVPKRVADYPIEW 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1766	100.0	864	11	Q60943 mus musculus
2	1254	71.0	866	11	Q43844 mus sapien
3	282.5	16.0	426	4	Q9NR14 mus sapien
4	280.5	15.9	502	4	Q9NRM6 mus sapien
5	247.5	14.0	499	11	Q9JIP3 mus musculu
6	231	13.1	288	4	Q9NRM5 mus musculu
7	140.5	8.0	218	11	Q9JIP2 mus musculu
8	112.5	6.4	708	3	Q9P7H9 xenopus lae
9	99.5	5.6	1506	13	P79927 human immun
10	97.5	5.5	328	14	Q9IU91 human immun
11	94.5	5.4	592	11	Q9JIN5 mus musculu
12	92	5.2	682	10	Q9FX72 arabidopsi
13	91.5	5.2	3131	3	Q42926 schizosacch
14	91	5.2	333	5	Q62453 caenorhabd1
15	89.5	5.1	1815	5	Q22531 caenorhabd1
16	88	5.0	1231	5	Q17024 anopheles 9
17	88	5.0	1333	3	Q13686 schizosacch
18	87.5	5.0	416	10	Q9SYG6 arabidopsi
19	87.5	5.0	1188	5	Q76326 drosophila

20	87	4.9	2515	5	Q9W2J8	Q9W2J8 drosophila
21	86.5	4.9	920	5	Q9YEB7	Q9YEB7 drosophila
22	86.5	4.9	947	14	Q9E964	Q9E964 ryegrass mo
23	85.5	4.8	356	2	Q9R221	Q9R221 vibrio chol
24	85.5	4.8	562	10	Q9SSG8	Q9SSG8 arabidopsi
25	85.5	4.8	1280	5	Q9YV47	Q9YV47 drosophila
26	85	4.8	925	4	Q9UJB2	Q9UJB2 homo sapien
27	85	4.8	985	4	Q9UJB3	Q9UJB3 homo sapien
28	85	4.8	1082	13	Q9PWC9	Q9PWC9 xenopus lae
29	84.5	4.8	712	10	Q80773	Q80773 arabidopsi
30	84.5	4.8	969	5	Q9VLL1	Q9VLL1 drosophila
31	84.5	4.8	1388	4	Q9NS87	Q9NS87 homo sapien
32	84	4.8	430	14	Q9WRE3	Q9WRE3 human immun
33	84	4.8	574	4	Q9P2L8	Q9P2L8 homo sapien
34	83.5	4.7	304	2	Q9I5A6	Q9I5A6 pseudomonas
35	83.5	4.7	432	14	Q9Q922	Q9Q922 shope fibro
36	83.5	4.7	880	5	Q9V4N0	Q9V4N0 drosophila
37	83.5	4.7	1349	11	Q9WV10	Q9WV10 rattus norv
38	83	4.7	868	11	Q9R094	Q9R094 mus musculu
39	83	4.7	431	4	Q15137	Q15137 homo sapien
40	83	4.7	4688	2	Q9PQ08	Q9PQ08 ureaplasma
41	82.5	4.7	399	14	Q92407	Q92407 bomblyx mori
42	82.5	4.7	565	2	Q47634	Q47634 escherichia
43	82.5	4.7	565	2	Q47635	Q47635 shigella fl
44	82.5	4.7	692	5	Q9W520	Q9W520 drosophila
45	82.5	4.7	1030	5	Q17443	Q17443 caenorhabd1

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	864 AA.
Q60943	Q60943	01-NOV-1996 (TREMBLrel. 01, Created)		
AC	Q60943	01-NOV-1996 (TREMBLrel. 01, last sequence update)		
DT	01-NOV-1996 (TREMBLrel. 01, last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, last annotation update)			
DE	INTERLEUKIN 17 RECEPTOR.			
GN	IL17R.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=THYMOMA EL4;			
RC	MEDLINE=96111968; PubMed=8777726;			
RX	Yao Z., Fanslow W.C., Seldin M.F., Rousseau A.M., Palinter S.L.,			
RA	"Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a			
RT	novel cytokine receptor."			
RL	Immunity 3:811-821(1995).			
DR	EMBL: U31993; AAC52357.1; -			
DR	MGI: 107399; IL17F.			
SQ	SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;			

Query Match 100.0%; Score 1766; DB 11; Length 864;
Best local similarity 100.0%; Pred. No. 5.9e-163; Indels 0; Gaps 0;
Matches 322; Conservative

QY	1	MAIRRCMPRVVPGALGWL	11	Q60943	mus musculus
DB	1	MAIRRCMPRVVPGALGWL	11	Q43844	mus sapien
QY	61	SWIHPKMLTPSSPKNTIYNLSVSTO	61	Q9NR14	mus sapien
DB	61	SWIHPKMLTPSSPKNTIYNLSVSTO	61	Q9NRM6	mus sapien
QY	121	TNERLCVKFQFLSMLOHHRKRWPFSE	121	Q9JIP3	mus musculu
DB	121	TNERLCVKFQFLSMLOHHRKRWPFSE	121	Q9JIP2	mus musculu
QY	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	Q9P7H9	xenopus lae
DB	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	P79927	human immun
QY	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	Q9IU91	human immun
DB	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	Q9JIN5	mus musculu
QY	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	Q9FX72	arabidopsi
DB	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	Q42926	schizosacch
QY	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	Q62453	caenorhabd1
DB	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	Q22531	caenorhabd1
QY	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	Q17024	anopheles 9
DB	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	Q13686	schizosacch
QY	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	Q9SYG6	arabidopsi
DB	180	IIIIIIIIIIIIIIIIIIIIIIIIIIII	180	Q76326	drosophila

QY 181 FVPCEDSKKMTTSCVSSGSLMDPNITVETLDTQHLRVDFETLMNESTPYOVLLSEFSDS 240
 DB 181 FVPCEDSKKMTTSCVSSGSLMDPNITVETLDTQHLRVDFETLMNESTPYOVLLSEFSDS 240
 QY 241 EHNHSCDVYKQIFAPROEFHORANVTFTLSKFMWCHHHVQVOPFSSCLNDCLRHAYT 300
 DB 241 EHNHSCDVYKQIFAPROEFHORANVTFTLSKFMWCHHHVQVOPFSSCLNDCLRHAYT 300
 QY 301 VPCPVISNTTVKRPVADYIPLM 322
 DB 301 VPCPVISNTTVKRPVADYIPLM 322

RESULT 2
 Q43844 PRELIMINARY: PRT: 866 AA.
 AC 043844:
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE IL-17 RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98035683; PubMed=9367539;
 RA Yano Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,
 Vandebos T., Zappone J., Painter S.L., Armitage R.J.,
 RT "Molecular characterization of the human Interleukin (IL)-17
 receptor."
 RT Cytokine 9:794-800(1997).
 RL EMBL: U56917; AAB99730.1; -
 DR SEQUENCE 866 AA; 96121 MW; 88AF626A83F3FE70 CRC64;
 SQ

Query Match 71.0%; Score 1254; DB 4; Length 866;
 Best Local Similarity 71.4%; Pred. No. 3.1e-113;
 Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

QY 1 MAIRRCMPRVGPALGWLILNLVLAAPRASPRLLDPAPVCAOEGLSGRVNSTCLDD 60
 DB 1 MGAARSPSPASVAPRLGLLILGLVLAAPRASPRLLDPAPVCAOEGLSGRVNSTCLDD 60
 QY 61 SWHPRNLPSSPKNIYINLSVSTOHELVPVLAHVEWTLQTDASILYLEGAEISVLQIN 120
 DB 61 SWHPRNLPSSPKNIYINLSVSTOHELVPVLAHVEWTLQTDASILYLEGAEISVLQIN 120
 QY 121 TNERLCVQFOFLSMLOHNRKRMRFSEHFVVDGQEVYVHHLPRIPDGDNRHKSIT 180
 DB 121 TNERLCVREFELSKLHNRHMRFTSHVVDQEVYVHHLPRIPDGDNRHKSIT 180
 QY 181 FVPCEDSKKMTTSCVSSGSLMDPNITVETLDTQHLRVDFETLMNESTPYOVLLSEFSDS 240
 DB 181 FVPCEDSKKMTTSCVSSGSLMDPNITVETLDTQHLRVDFETLMNESTPYOVLLSEFSDS 240
 QY 241 EHNHSCDVYKQIFAPROEFHORANVTFTLSKFMWCHHHVQVOPFSSCLNDCLRHAYT 300
 DB 241 EHNHSCDVYKQIFAPROEFHORANVTFTLSKFMWCHHHVQVOPFSSCLNDCLRHAYT 300
 QY 301 VPCPVISNTTVKRPVADYIPLM 322
 DB 301 VPCPVISNTTVKRPVADYIPLM 322

DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE IL-17 RECEPTOR.
 GN IL17BR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20317118; PubMed=10749887;
 RA Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,
 RA Barber M.C., Wang W., Mathen K., Hodge V., Fisher C.L., Olsen H.,
 RA Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,
 RA Carrell J.A., Ebner R.J.
 RT "A novel cytokine receptor-ligand pair. Identification, molecular
 RT characterization, and in vivo immunomodulatory activity."
 RL J. Biol. Chem. 275:19167-19176(2000).
 DR EMBL: AF212365; AAF78776.1; -
 KW Receptor.
 SQ SEQUENCE 426 AA; 47137 MW; D5B820CCEFC12E27 CRC64;

Query Match 16.0%; Score 282.5; DB 4; Length 426;
 Best Local Similarity 28.2%; Pred. No. 3e-19;
 Matches 89; Conservative 50; Mismatches 138; Indels 39; Gaps 11;
 QY 20 LLLNLVLAAGR-ASPRLLDPAPVCAOEGLSGRVNSTCLDDSWHPRNLPSSPKNIYI 78
 DB 3 LVLLSLAALCRSAVPR---EPTVCGSE-----TGSPKEMQLHDLRGLRLRY 50
 QY 79 NLSVSTOHELVPVLAHVEWTLQTDASILYLEGAEISVL-QLNTNERLCVQFOFLSMLOH 137
 DB 51 EPVTVATGTDYSILTMVNSVLRADASIRLKATKICVTGKSNFQSYCYVCNTEAFQ 110
 QY 138 HRK---RMRFSEHFVVDGQEVYVHHLPRIPDGDNRHKSITFYVDCEDSKKMT 193
 DB 111 QTRPSGKMTFSYIGFVENVLYFIQAHNIPRANMDESPSVNFTSGCCLDHITKRY 170
 QY 194 TSCVSSGSLMDPNITVETLDTQHLRVDFETLMNESTPYOVLLSEFSDSEHNHSCDVYKQIF 253
 DB 171 KCKVAGSLMDPNITACKKNEETVEVFTTPLGNRMALID-----HSTLIGFSQVE 223
 QY 254 APROEFHORANVTFTLSKFMWCHHHVQVOPFSSCLNDCLRHAYTV-CPVISTVTP 312
 DB 224 EPHQRK-QTRASVIVPYTGSEGA--TVQLTFYPTCGSDCLNKGTVVLCP---QTGVP 277
 QY 313 KRY-----ADYIPL 321
 DB 278 FPLDNKSKRGGWLP 293

RESULT 4
 Q9NRM6 PRELIMINARY: PRT: 502 AA.
 AC 09NRM6:
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE IL-17 RECEPTOR HOMOLOG PRECURSOR.
 GN EVI27.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20273223; PubMed=10815801;
 RA Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
 RA Shughnessy J.D., Jr.,
 RT "EVI27 encodes a novel membrane protein with homology to the IL17
 receptor."
 RT Oncogene 19:2098-2109(2000).
 RL EMBL: AF208110; AAF86051.1; -

Db 281 ALLPADT 287

RESULT 7

ID 09JIP2 PRELIMINARY; PRT; 218 AA.

AC 09JIP2; PRELIMINARY; PRT; 218 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE IL-17 RECEPTOR HOMOLOGY SHORT ISOFORM PRECURSOR.

GN EVI27.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20273223; PubMed=10815801.

RA Tian E., Sawyer J.R., Largeaspa D.A., Jenkins N.A., Copeland N.G.,

RA Shaugnessy J.D. Jr.;

RT "EVI27 encodes a novel membrane protein with homology to the IL17

receptor."

RL Oncogene 19:2098-2109(2000).

DR EMBL; AF208109; AAF6050.1;

DR InterPro; IPR002259;

DR ProDom; PD005103; ; 1.

KW Signal; Receptor.

FT SIGNAL 1 8

FT CHAIN 9 218

FT SEQUENCE 218 AA; 23855 MW; E17C15AC824E1F0B CRC64;

SQ

Query Match

Best Local Similarity 24.6%; Score 140.5; DB 11; Length 218;

Matches 45; Conservative 32; Mismatches 87; Indels 19; Gaps 5;

Db 19 LLLIANTLAFG--RASPRLLDFPAPVCAQGLSCRVKSTCLDSDSWHPKNTLPPSSPKNI 76

Db 1 MLVLLIILAAASCSALPR---EPTIOGSGE-----TGPSEEMVVOHTLPDGLRDL 48

QY 77 YINLSVSTGHGELVPLVHLEWTLQDASITLYEGAEISVL-QLNTNERLCVRFQETLSML 135

Db 49 QVLYVTSVAAEFSTILMNISWILRADASTIRLKAIRICVSGKNNMNSVCVACNTENF 108

QY 136 QHHRK---RWRFSSHFFVVDPGOEYEVTVHLPKPIPDGDPHKSKIIIFVPCEDSKMK 191

Db 109 OSQTRPSGKWFPSYVGPVELSTLILSHNIPNANMNDSPSLSVNFTSPCTRENT 168

QY 192 MTT 194

Db 169 VTS 171

RESULT 8

ID 09P7H9 PRELIMINARY; PRT; 708 AA.

AC 09P7H9; PRELIMINARY; PRT; 708 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE PUTATIVE TRANSCRIPTIONAL ACTIVATOR.

GN SPAC105.03C.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OC NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972H-;

RA Harris D., Wood V., Rajandream M.A., Barrell B.G.;

SQ Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL157994; CAB76236.1; -.

DR InterPro; IPR003015; -.

DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN.1.

SQ SEQUENCE 708 AA; 80989 MW; 78F57C5A0EB2DE76 CRC64;

Query Match

Best Local Similarity 21.6%; Score 112.5; DB 3; Length 708;

Matches 63; Conservative 45; Mismatches 78; Indels 105; Gaps 15;

Db 44 ADEGICSRVKNSTCL-----DSDWHPKNTLPPSSPKNIYINL-----SV 82

Db 14 AQPNCICPSCSLTCLIHHERFSSSFMDPVSLFCSSP---YPNLPKRRSSSLSKKPSV 70

QY 83 SS-----TQGEVLVPLAVE---WTLOTASITLYEGAEISVLQNTNERLCV 127

Db 71 ASQDKSDGTLPDIGNNPLIPSHQESSHWITIRHESMPSALAGSSAQSMQ----- 121

QY 128 KFOPLSMLOHHRK-RWRFSSHFFVVDPGOEYEVTVHLPKPI-----PDGDPHKSKII 180

Db 122 --QPSITQNNENRFRKSFQO-----PPYVETTFPVKSEPEQEHAKL 163

QY 181 -----FVPCEDSKKMT-----SCVSGSLMDPNITV-----ETLDTOLRVDFTL 223

Db 164 SDLSYEFELKYSSTKVERSEAPPPSSLNSTVLDENDSLISOGSSVDQ---TDFTLG 220

QY 224 WNESTPYQVLESFSDSENSHSCFDVVKQIFAPQOEFRHORANTFTLSKPH 274

Db 221 FDDSLSYAVIILNPTSDSD---VDLIRQYFIKREG-----TYFTFSNMH 259

RESULT 9

ID P79927 PRELIMINARY; PRT; 1506 AA.

AC P79927; PRELIMINARY; PRT; 1506 AA.

DT 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE INTEGUMENTARY MUCIN B.1 (FRAGMENT).

GN FIM-B-1.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

OC Xenopodidae; Xenopus.

OC NCBI_TaxID=8335;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SKIN;

RX MEDLINE=97153143; PubMed=8999864;

RA Joda W., Hoffmann W.;

RT "Similarities of integumentary mucin B.1 from Xenopus laevis and

prepro-von Willebrand factor at their amino-terminal regions."

RL J. Biol. Chem. 272:1805-1810(1997).

DR EMBL; Y08296; CAA69604.1; -.

DR HSSP; P19398; 1ATB.

DR InterPro; IPR000436; -.

DR InterPro; IPR001846; -.

DR InterPro; IPR002919; -.

DR Pfam; PF00084; sush1; 1.

DR Pfam; PF00094; wvd; 3.

DR Pfam; PF01826; TIL; 1.

DR SMART; SM00032; CCP; 1.

DR NON_TER 1506

FT SEQUENCE 1506 AA; 163905 MW; 7BF269A748DC817F CRC64;

SQ

Query Match

Best Local Similarity 5.6%; Score 99.5; DB 13; Length 1506;

Matches 63; Conservative 35; Mismatches 110; Indels 91; Gaps 16;

Db 56 TCLDDSWIHKKNTLPSSPK---NIYINL---SVSSTQHGELVPLV---LHVMK----- 98

Db 495 TCGNGTWTCSKSGCPGICKVEEGVYVTTDGIITYSMHGNCVYIISHTSMYVYAKLSQSO 554

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QY 99 -----TLQTDASILEGAEISVLQLN-----TNERLCVKRQ-----FLSML 135
DB 555 DAQSTIINSVSLVNLGNQESTYTFNRDQSLINEKTNQNVFQSDLSISRQSTFIIVL 614
QY 136 OHRRKRMR-----SFHFVVDGQGEYVYVHLPRKPIPDGDPNHNKSKIIIVPDCDSKMK 191
DB 615 TNLHVNLIIQTGTMOFYTSVPSTGYEDTEG-----PCGSFNHKKADDDPM-----SNOK 663
QY 192 MTTSCVSSGSLMDPNTVETLDTQHLRVDFTLNNESTPYQVLESPDSFNHSCDFVVKO 251
DB 664 M-----PSSPETF-----VGF--WK-----WSSCSDPYKPTCIDLEKE 695
QY 252 IFAPROEEHORANVTFTLSKFMCHHVVQVOPFFSSCLN-DCLRHAATVP-CPVISM 308
DB 696 LFANQOCQSLKDPNGAFAR-----CHSTVLYKRSFYERCVHLNCISQDMVVMCTELRN 748

RESULT 10
Q91091 PRELIMINARY; PRT; 328 AA.
AC Q91091:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE EXTERIOR MEMBRANE PROTEIN GP120 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96NG-MACSW031;
RX MEDLINE=20179113; PubMed=10716369;
RA Peeters M., Bsu-Williams E., Vergne L., Montavon C.,
RA Mulanga-Kabeya C., Harry T., Idilonke A., Lesage D., Patrel D.,
RA Delaporte E.;
RT "Predominance of subtype A and G HIV type 1 in Nigeria, with
RT geographical differences in their distribution.";
RL AIDS Res. Hum. Retroviruses 16:315-325(2000).
DR EMBL; AJ389751; CAB77485.1; -.
DR InterPro; IPR000777; -.
DR Pfam; PF00516; GP120; 1.
FT NON_TER 1
FT SEQUENCE 328 AA; 36504 MW; DE92C03A75CF898E CRC64;

Query Match 5.5%; Score 97.5; DB 14; Length 328;
Best Local Similarity 22.2%; Pred. No. 0.21;
Matches 70; Conservative 32; Mismatches 85; Indels 129; Gaps 18;
QY 20 LLLNLVLAAGRASPRLDPPAPV-CAQEG--LSCRKVN---STCLDDSWIHPKMLTP 70
DB 64 LINCUNVSAINQACPKVSPRIPHYCAPAGAFALICRDKNKGNGTCT----- 110
QY 71 SSPKNITVILSVSTQ--HGLVPLVHVEWTL-----QTPASTL--YLGAELSVQLN 120
DB 111 -----KIVSYVQCTHG-IPVAVSTQLLNGSLAEEDIVIRTEYNTNNAKIIIVQLN 160
QY 121 -TNERLCVFCFTSLMLOHRRKRMSFSHFVVDGQGEYVYVHLPRKPIPDGDPNHNKSKI 179
DB 161 ETIELNCTPRN-----NNTKRKSIRFG-----PGQAFYAT-----GD----- 191
QY 180 IFVPCDEDSKMMKMTTSCVSSGSLMDPNTVETLDTQHLRVDFTLNNE--STPYQV-LLE 235
DB 192 -----IENIRQAHCHNVSPRTKMNMIMQIKVQVQLKRIE 223
QY 236 SFS-----DSEHSCFDVYKQIFAPROEEHORANVTFTLSKFMCHHVVQVOPFFSS 289
DB 224 SFRKNKINSFSSSGGLEITTHSFCNGRGEFFYCYNTSELFTKN-----ST 267
QY 290 CLNDCLRHAATVP 305

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DB 268 SKNST--TITLPCRI 280

RESULT 11
Q91JN5 PRELIMINARY; PRT; 592 AA.
AC Q91JN5:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE ERYTHROID MEMBRANE ASSOCIATED PROTEIN ERMAP.
GN ERMAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10990;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20184753; PubMed=10721728;
RA Ye T.-Z., Gordon C.T., Lai Y.-H., Fujiwara Y., Peters L.L.,
RA Perkins A.C., Chui D.H.K.;
RT "Ermap, a gene coding for a novel erythroid specific adhesion/receptor
RT membrane protein.";
RL Gene 242:337-345(2000).
DR EMBL; AF153906; AAF31162.1; -.
DR InterPro; IPR000107; -.
DR InterPro; IPR001211; -.
DR InterPro; IPR001870; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00622; SPRY; 1.
DR PRINTS; PRO1407; B0TYPHNDUF.
DR PRODOM; PD000303; -.
DR SMART; SMO0406; IgV; 1.
SQ SEQUENCE 592 AA; 66555 MW; 246AC691B8788B8 CRC64;

Query Match 5.4%; Score 94.5; DB 11; Length 592;
Best Local Similarity 21.9%; Pred. No. 0.8;
Matches 69; Conservative 39; Mismatches 112; Indels 95; Gaps 15;
QY 65 PKNLTPSSPKNITVILSVSTQHGELVPLVHVEWTLQTDASTIYLEGAEISVLQNTNER 124
DB 263 PERGSLSSPA--VALSV-----VLPVL-----GLITLGIWLICKOKSKER 302
QY 125 LCVK--FOFLSMLQHRRK-----WRFSSHFV--VDPG 154
DB 303 LIYEQAMEVESILEHNAKEKRLHAKLKLRLSELKLRANAANGWRARLHVAATVLDLD 362
QY 155 QEYE-----VTVHLPRKPIPDGDPNHNKSKIIIVPDCDSKMMKMTSC-----VS 198
DB 363 TAPRLILSEDRRCVRLGDRKRVPVD-NPERFDEVVSVGSE-----YFTTGHYWEVYVG 417
QY 199 SGLMDPNTVETLDTQ-----HLRVDFTLNNESTPYQVLE--SFDSFNHSC 245
DB 418 EKTAKIILGVCSSESYSVRKGVATSPANGHVLVROSQNE--YEALTSPTSFTLKSPPC 474
QY 246 FDVYKQIFAPROEEHORANVTFTLSKFMCHHVVQVOPFFSSCLNDCLRHAATVP 305
DB 475 VG-----IFLDYEAGIISRYNTDKSHIFFTTSFSSPLRPFEPCLHDGCKNT----APL 526
QY 306 ISNTVPRPVADYIP 320
DB 527 IICTELQKSESIYP 541

RESULT 12
Q9FX72 PRELIMINARY; PRT; 682 AA.
AC Q9FX72:

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DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE F19K19.13 PROTEIN.
 GN F19K19.13
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Federici N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altair H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
 RA Buehler E., Chao Q., Chin C., Choi E., Gonzalez A.,
 RA Hong B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
 RA Lenz C., Liu A., Liu S., Mukharly N., Pham P., Sakano H., Shinn P.,
 RA Toriumi M., Vayberg M., Yu G., Ecker J., Theologis A., Davis R.W.,
 RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC011808; AAG10824.1;
 SQ SEQUENCE 682 AA; 77036 MW; D5713DF18EA87D94 CRC64;

Query Match 5.2%; Score 92; DB 10; Length 682;
 Best Local Similarity 22.98; Pred. No. 1.6;
 Matches 71; Conservative 36; Mismatches 109; Indels 94; Gaps 17;

QY 66 KNLTPS-----SPKNTINLSVSTGHE--LTPVLYHEWTLQ-----101
 DB 269 KSLRPSAIVMTHTSTIYVKKQLQRHNGAAYCVLYSENLSSHSGPVVTENLKR 328
 QY 102 TDASTL-YLEG---AELSVLQNTNERLC-----VKFOFLSMLOHRRR 141
 DB 329 PDGSMFGLYEVEKTLASGLQIRAG-HICWMDNDVYNGKPGAVRSPGYMSTFEDAKF 387
 QY 142 WRFSESHVVDPGQYEVTV--HILPKPIPDG-----PHKSKITIV--PDCEDEK 189
 DB 388 IDFIITSSAPSKTKGNGTVSGRPQ--LPSDELSEKSPSPHLYKSTIVYPIKSCAFS 446
 QY 190 MKMTTSCVSSGSLMDPNTVETLDTQHLRVDFTLNNESTPYOVLLESFSD-----SEN 242
 DB 447 VTRMPLC-RTGLHREMMVQGLTGE-----ILQKKRPEKSLIKFTDLERGLLSVES 499
 QY 243 HSCDD-----VKKQFAPROEEFHORANVT-----FTLSKFMCHHVOVOP 285
 DB 500 SRCEDEKHIRIKSDSYNPRNDEFDSHANILENRETRINRWFMTAIGROC-----KLIR 554
 QY 286 FESSGLNDCL 295
 DB 555 YSSSTSKDCL 564

RESULT 13
 042926 PRELIMINARY; PRT; 3131 AA.
 AC 042926;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-JUN-1998 (Tremblrel. 06, Last annotation update)
 DE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN.
 GN SPBC16C6.02C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=972H-;
 RA Purnelle B., Goffeau A., Wood V., Lyne M., Rajandream M.A.,
 RA Barrell B.G.;
 RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL02167; CAA16910.1;

SQ SEQUENCE 3131 AA; 354021 MW; BBD22BE7F668EEF4 CRC64;

Query Match 5.2%; Score 91.5; DB 3; Length 3131;
 Best Local Similarity 20.68; Pred. No. 11;
 Matches 68; Conservative 54; Mismatches 125; Indels 83; Gaps 15;

QY 17 GMLLLINLVAPGRASP-----RLDFF-----PAPVCAOERLSCRVNSTCLDSW 62
 DB 1898 GYVPLDLACLPLRLIRVRSKGLFLMSNQIVDMHLNKSPL--QYLCESTISWKHLL 1954
 QY 63 IHPKNTLPSSPKNTI-----INLSV-----STQHGELVP 92
 DB 1955 VFARNLMDGSLQNDVLPLOLNIPTLQIENILPYEINRIIERSGNDWRSSLSFGDLP 2014
 QY 93 VLVH-----EMTLQ-TDASTLY--EGAEVSLQNTNE-----RLCKKF 129
 DB 2015 ILHTDSKSFLLMGINVPDLQPVLDLPITYPISSGQVQTSALTSDKODVYKLLTKY 2074
 QY 130 QFLSMLOHHRKRMRFSESHVVDPGQYEVTV-----HILPKPIPDGPNHRSKILIEVPD 184
 DB 2075 EKLPGTNYVSK--VMIRPYIENHTLSIGVTSSPSISIVTIPSGSYNDIKPYFSF 2132
 QY 185 CEDSKMKTSCVSSGSLMDPNTVETLDTQHLRVDFTLNNESTPYOVLLESFSDSENHS 244
 DB 2133 DESGRKRRAMISIDNGTWSADIGFTLIGSSS-QVEVKTNES--DVCLIGMSISESSG 2188
 QY 245 CFQVVKQI-FAPROEEFHORANVTETLSKF 273
 DB 2189 KFCILKTSVTFTR-FVRKNHLDCTVSLREF 2217

RESULT 14
 062453 PRELIMINARY; PRT; 333 AA.
 AC 062453;
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)
 DE Y44AC.2 PROTEIN.
 GN Y44AC.2
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ainscough R.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94150718; PubMed-7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., Murray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smalton D., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Wellstock L., Wilkinson-Spratt J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RL Nature 368:32-38(1994).
 DR EMBL; AL021489; CAA16370.1;
 SQ SEQUENCE 333 AA; 38801 MW; 8B6CC20CE156DFEC CRC64;

Query Match 5.2%; Score 91; DB 5; Length 333;
 Best Local Similarity 20.28; Pred. No. 0.89;
 Matches 59; Conservative 44; Mismatches 105; Indels 84; Gaps 13;


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Oy      50  CRYANSCILD-----DSMHP-----KNLSPSSKNIIYNLSVSTQHGELVPLAH 96
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      50  CDSEBNSLDVRNSHQOLKSMISTEKIQLPFTLTIRTOVPRM-----IALLDL 102
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      97  EWTLOTDAISILEG---AELSVLOTNTNERLCVFOFL-----SMLOHRRKMRFSF 146
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      103  ETALPKTCVDLIIONVYAEADMRQOESVD-----OFMKCHIREGVLLH--EYVYNSP 154
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      147  SHFVVDPCQGEYEVVNLKPIPGCDENHNSKIIFV--PCEDESKMKMTTSCVSSGS-- 201
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      155  KMFOLD-----YLSVTSDDMKVPRDDELEMKKIYYLIDKSPFYSDNQFLRELKSGSSH 209
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      202  -----LMDPNITVEFLDTQHLKRVDEFTLNNESTPYOVLLESFSDSENHSCFD 247
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      210  RLQILISIOGNSMONTYWPDSVLTLEINAE-----LWNOETERNO--HYFLINAEHRKFK, 259
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      248  VKVOIGFAPRQGEFQRANVTFTLSKFMWCSHHNVQVOPRFFSCCINDCTIRAV 299
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      260  KIANHFYRDDQD-----GFGAELEHGVDLSLEARDFLKNQDGTIRSV 299
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 15

AD	Q22531	PRELIMINARY;	PTT; 1815 AA.
AC	Q22531;		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)	
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)	
DE	T16G12.1	PROTEIN.	
GN	T16G12.1.		
OS	Caenorhabditis elegans.		
CC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditioidea		
CC	Rhabditidae; Pelodierinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Thomas K.;		
RL	Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; Z30317; CA882971.2; -.		
DR	InterPro; IPR000130; -.		
DR	InterPro; IPR001117; -.		
DR	InterPro; IPR001930; -.		
DR	Pfam; PF01433; Peptidase_M1; 3.		
DR	PRINTS; PRO0756; ALADIPYASE.		
DR	PROSITE; PS00079; MULTICOOPER_OXIDASE1; UNKNOWN_1.		
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_2.		
SO	SEQUENCE	1815 AA; 207455 MW; 73EF51E9CA0359E9 CRC64;	

Query Match	5.1%;	Score	89.5;	DB	5;	Length	1815;
Best Local Similarity	21.2%;	Pred. No.	9;				
Matches	65;	Conservative	44;	Mismatches	108;	Indels	89;
				Gaps	15;		

[illegible]

QY	270	LSKFHW	275
		:	
Db	1649	VSKFQW	1654

Search completed: July 17, 2001, 11:20:41
job time: 160 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 17, 2001, 11:18:26 ; Search time 16.71 Seconds
(without alignments)
660.100 Million cell updates/sec

Title: US-09-488-728-2_COPY_1_322
Perfect score: 1766
Sequence: 1 MAIRRCMPRVPGPALGWL.....CPVISNTVPKPVADYIPLW 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query length	ID	Description
1	101	5.7	880 1 TYO3_RAT	P55146 ratu
2	99	5.6	449 1 GAD_MOUSE	P22933 mus
3	98	5.5	1748 1 YNR2_YEAST	P53886 sac
4	97	5.5	880 1 TYO3_MOUSE	P55144 mus
5	95	5.4	449 1 GAD_RAT	P18506 ratu
6	94	5.3	388 1 GMCR_MOUSE	Q00941 mus
7	89.5	5.1	606 1 PR20_CHIRE	P93107 chl
8	88.5	5.0	954 1 YH9_YEAST	P38138 sac
9	87	4.9	452 1 GAD_HUMAN	O14764 hom
10	87	4.9	520 1 CPE2_HUMAN	P78329 hom
11	87	4.9	2515 1 TUD_DROME	P25823 dro
12	86.5	4.9	377 1 ICE4_HUMAN	P49662 hom
13	86	4.9	2569 1 LMA3_MOUSE	O61789 mus
14	85.5	4.8	1164 1 DP3A_VIBCH	P52022 vib
15	85	4.8	925 1 DBL_HUMAN	P10911 hom
16	84.5	4.8	429 1 EPC_RAT	P01855 ratu
17	84.5	4.8	455 1 ZPRL_CAERE	O16999 cae
18	83.5	4.7	1213 1 T2D2_DROME	Q24325 dro
19	83	4.7	432 1 BRAC_XENLA	P24781 xen
20	83	4.7	672 1 KPCC_HUMAN	P17552 hom
21	83	4.7	672 1 KPCC_RABIT	P10102 cry
22	83	4.7	1038 1 TRAA_HUMAN	P05696 ratu
23	83	4.7	1038 1 TRAA_HUMAN	P13612 hom
24	82.5	4.7	329 1 GGC_RAT	P20762 ratu
25	82	4.6	672 1 KPCC_BOVIN	P04409 bos
26	82	4.6	808 1 POLG_HPVC	Q02381 hep
27	81.5	4.6	852 1 POLG_HPVC	P06442 hep
28	81.5	4.6	1134 1 IF3X_HUMAN	O75153 hep
29	81.5	4.6	1152 1 ITAM_HUMAN	P11215 hom
30	81	4.6	510 1 VIL_HPV22	P50788 hum
31	81	4.6	672 1 KPCC_MOUSE	P20444 mus
32	81	4.6	839 1 POLG_HPAVT	P31788 sim
33	80.5	4.6	421 1 EPC_MOUSE	P06336 mus

34	80.5	4.6	2347 1	KROS_HUMAN	P08922 homo sapien
35	80	4.5	666 1	2P2_RABIT	P48829 oryctolagus
36	79.5	4.5	392 1	BM15_HUMAN	O95972 homo sapien
37	79.5	4.5	658 1	KPC1_LYTP1	O25378 lytechinus
38	79.5	4.5	716 1	2P2_PIG	P42099 sus scrofa
39	79	4.5	488 1	PHR_SYNY3	Q05081 synechocyst
40	79	4.5	745 1	2P2_MACRA	O77726 macaca radi
41	79	4.5	887 1	BCM2_DROME	P49735 drosophila
42	79	4.5	3418 1	BRG2_HUMAN	P51587 homo sapien
43	79	4.5	3712 1	IMA_DROME	O00174 drosophila
44	78.5	4.4	377 1	ICED_HUMAN	O75601 homo sapien
45	78.5	4.4	450 1	COPP_MOUSE	O55029 mus musculus

ALIGNMENTS

RESULT 1
ID TYO3_RAT STANDARD: PRT; 880 AA.
AC P55146;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (EC 2.7.1.112)
GN TYRO3 OR SKY.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=9610499; PubMed=7490270;
RA Onishi K., Honda S., Ichinomiya N., Nakamura T., Mizuno K.;
RT "Molecular cloning and in situ localization in the brain of rat sky
receptor tyrosine kinase.";
RL J. Biochem. 117:1267-1275(1995).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
IN THE CENTRAL NERVOUS SYSTEM.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN
OTHER TISSUES.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D37880; BA07119.1; -;
DR HSSP: P11362; IREG1.
DR InterPro: IPR000719; -;
DR InterPro: IPR001245; -;
DR InterPro: IPR001777; -;
DR InterPro: IPR003006; -;
DR Pfam: PF00047; fn3; 2.
DR Pfam: PF00069; pkinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
Transferase; Phosphorylation; Transmembrane; Signal; Repeat;

QY 16 LGWLLLLNLVLAAGRASPRLDEPAVCAOEGLSCKVN-----STCLDDSWI----- 63
 Db 4 LGWLL-----PLLL-----LCQPHHGARAMNDIGYVSNLEISMLPNIDGL 47
 QY 64 ---HKRNLTP---SSPKNIYINLSVSTOGEVLVPLVHWMTLOTDAISILYLEGAEISVL 117
 Db 48 MEGYARNFRPGIGGAPVNVALLALEVASIDH---ISEANNEYTMV---FLHQSWRSRLS 101
 QY 118 QLNTNERLCVKFOPLSMLOHHRKRWRFSESHFVYDGOE--YEVTVHH-LPKPIPDGPN 174
 Db 102 YNHTVETIGLDRFPDKL-----WLPDPTIVNAKSAHFHYTVENKIRIQPDG--- 150
 QY 175 HKSKTIFFVDDCEDSKMKMTSCVSSGLMDPNITVEITDQHLRVDTLWNESTPYOVL 234
 Db 151 ---VILY-----SIRTSIVAC-----DMDLAKYPLDQECMLD-----L 182
 QY 235 ESFSSEHNHSCFDYVKQIAPROEPH-----QNAVTFILSKF 273
 Db 183 ESY-----GTSSEDIY-YWSENQEOIHGLRLQLAQFTTYSRF 221

RESULT 3

YNR2_YEAST 3
 ID YNR2_YEAST STANDARD: PRT: 1748 AA.
 AC P53886;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE HYPOTHELTAL 196.1 KDA PROTEIN IN RPS3-PSDI INTERGENIC REGION.
 GN YNL172W OR N1677.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;

RM [1]
 RP SEQUENCE FROM N.A.
 RA Obermiller B., Piravandi E., Rinke M., Domdey H.;
 RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
 CC -1 SIMILARITY: TO A.NIDULANS BIME AND MOUSE TSG24.

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 CC or send an email to license@sib-sib.ch).

DR EMBL; 271448; CA96060.1;
 DR SGD; S0005116; YNL172W.

DR Hypothetical protein: Transmembrane.

FT TRANSMEM 1378 1398 POTENTIAL.
 SQ SEQUENCE 1748 AA; 196142 MW; 34BC9212020BB2B5 CRC64;

Query Match 5.5%; Score 98; DB 1; Length 1748;
 Best Local Similarity 22.9%; Pred. No. 3.1;

Matches 69; Conservative 38; Mismatches 104; Indels 90; Gaps 16;

QY 29 GRASPRLLDFAFAP-VCAOEGLSGSC---RYKNSSTCLDSDWTHPKMLTPSSPKNIYINLSVSS 84
 Db 289 GNASGRTDIFALPSSCSRSRLSATLDRMGN-----IAPTN-RAAPSGFTDSSANT 339
 QY 85 TONGELVYV-----LHWMTLOTDAISILYLEGAEISVLQN-----TNERL---CVKFO 130
 Db 340 ATHSHITPVSPMQOQOQOQYLNQATSSKDIYLTETISSLKLPDDIIFTSRRLSILSKLK 399
 QY 131 FLTSM-----OHHRKRWRFSESHFVYDGOEVEVYVHHLPKPIPDGDPYHKS 177
 Db 400 FLSTLFRREGILLIHEPHFKIWLIDLPVLD-----SIFPKIYGNSPQNM 449
 QY 178 KIIFVDDCEDSKMK-----MTTSC---VSSGS-----LWDPNITVEITD 214

Db 450 RL-----ENLKEPSRIQAMYIHLLLESCILIVSECONKEEKAKLYDPFKI-TSPS 502
 QY 215 QHLRVDTFLMNSTPYQVLLSEFSDSSENSHSCFDYVKQIAPROEPHQAQNAVTFILSKFH 274
 Db 503 KNISEELTKONSLPQLKLPETSTFKLCFVAVYITSP-----AFNISFT---FL 552
 QY 275 W 275
 Db 553 W 553

RESULT 4

TYO3_MOUSE 4
 ID TYO3_MOUSE STANDARD: PRT: 880 AA.
 AC P51144;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (BC 2.7.1.112)
 DE (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).
 GN TYRO3 OR DTK OR RSE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RM [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=94193774; PubMed=7511603;
 RA Mark M.R., Scadden D.T., Wang Z., Gu Q., Goddard A., Godowski P.J.;
 RT "RSE, a novel receptor-type tyrosine kinase with homology to Axl/Ufo,
 RT is expressed at high levels in the brain.";
 RL J Biol. Chem. 269:10720-10728(1994).

RM [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=95161079; PubMed=7857657;
 RA Crosier P.S., Lewis P.M., Hall L.R., Vitas M.R., Morris C.M.,
 RA Beier D.R., Wood C.R., Crosier K.E.;
 RT "Isolation of a receptor tyrosine kinase (DTK) from embryonic stem
 RT cells: structure, genetic mapping and analysis of expression.";
 RL Growth Factors 11:125-136(1994).

RM [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=94336210; PubMed=8058320;
 RA Lai C., Gore M., Lemke G.;
 RT "Structure, expression, and activity of Tyro 3, a neural adhesion-
 RT related receptor tyrosine kinase.";
 RL Oncogene 9:2567-2578(1994).

RM [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RX MEDLINE=95240399; PubMed=7723626;
 RA Schulz N., Paulhac C., Lee L., Zhou R.;
 RT "Isolation and expression analysis of tyro3, a murine growth factor
 RT receptor tyrosine kinase preferentially expressed in adult brain.";
 RL Brain Res. Mol. Brain Res. 28:273-280(1995).

RM [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RA Sasaki M.;

RL Submitted (JUN-1995) to the EMBL/Genbank/DBJ databases.
 CC -1 FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
 CC IN THE CENTRAL NERVOUS SYSTEM.

CC -1 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.

CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1 TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN
 CC OTHER TISSUES.

CC -1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
 CC AXL/UFO SUBFAMILY.

```
CC CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR DR EMBL; U05683; AAA19237.1; -.
DR DR EMBL; U18933; AAC52148.1; -.
DR DR EMBL; X78103; CAAS495.1; ALT_INIT.
DR DR EMBL; U18342; AAB26942.1; ALT_INIT.
DR DR HSP; P11362; IFCI.
DR DR MGD; MG1:104294; TYRO3.
DR DR InterPro; IPRO00719; -.
DR DR InterPro; IPRO01245; -.
DR DR InterPro; IPRO01777; -.
DR DR InterPro; IPRO03006; -.
DR DR Pfam; PF00041; fn3_2.
DR DR Pfam; PF00047; ig_2.
DR DR Pfam; PF00069; PKinase_1.
DR DR PROSITE; PS00107; PROTEIN_KINASE_ATP_1.
DR DR PROSITE; PS00109; PROTEIN_KINASE_TYR_1.
DR DR PROSITE; PS50011; PROTEIN_KINASE_DOM_1.
KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KM Transferrin; Phosphorylation; Transmembrane; Signal; Repeat;
KV Immunoglobulin domain.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 880 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3.
FT DOMAIN 31 419 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 420 440 POTENTIAL.
FT DOMAIN 441 880 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 47 114 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 143 200 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 214 301 FIBRONECTIN TYPE-III.
FT DOMAIN 305 401 FIBRONECTIN TYPE-III.
FT DOMAIN 401 785 PROTEIN KINASE.
FT NP_BIND 508 785 ATP (BY SIMILARITY).
FT BINDING 514 522 ATP (BY SIMILARITY).
FT ACT_SITE 540 540 ATP (BY SIMILARITY).
FT ACT_SITE 645 645 BY SIMILARITY.
FT DISULFID 54 107 BY SIMILARITY.
FT DISULFID 150 193 BY SIMILARITY.
FT CARBOHYD 53 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 370 370 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 676 676 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 630 630 A -> R (IN REF. 3).
FT CONFLICT 811 811 L -> V (IN REF. 3).
SQ SEQUENCE 880 AA; 96222 MW; 3B7AC36CB016B3F7 CRC64;

Query Match 5.5%; Score 97; DB 1; Length 880;
Best Local Similarity 21.0%; Pred. No. 1.6;
Matches 77; Conservative 55; Mismatches 126; Indels 108; Gaps 20

QY 1 MAIRRC-WPRVVPGPALGWL--LLNVLAGRASP-RLLDFRPVCAGDS-----LSG 50
   ||| | | : | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MALRRMGWPGGRP-----LLLAGLASLLFGSAAAGIKMGAPKMTVSQGYPVKLNC 54
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 51 RKNSNGCLDDSSNIHKNLPPSSPKNTYINLVSSYSDHGEVLPAIVHEWTLOTDPASTILE 110
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 55 SVEGMEDPPIHHMKDKGTYYQNASQ-----VSISISH-SWIGLLSLKYSERSDAGLYWCQ 108
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 111 GAELSVLTQNTNERLCVKRFQLSMQLQHHRKRWFSESHFVVDP----- 153
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Db      109 VKDEEFTKISOSWALIVE-----GVPEFTVEFDLAVPNAPFOLSCSEA 152
QY      154 -GGEYETVHLLPPIPGDGNHKSIIFFP-----DCEDESKM-MTSCVSSGSLW 203
Db      153 VGPEPEPTIYMWRLGTLKVGAPSPSVLNTGVQRTFEESEANNKIGLARSRAIYRLQ 212
QY      204 DP-----NIIVETLDTOHLRVDFTLNNESTIYOVULESFSESNHSCPDYVKQIFAPROE 258
Db      213 APPAPFETVITVITISSYNASV---AWPVGADGALL-----HSC--TVQVNAHP--G 257
QY      259 EEFHORANTFLLSNFHHCHHHVOYOFPESSC-----LNDCLRHAVTYVCPVISTMTYVKP 314
Db      258 EWEALAAV-----VPVPPF--TCLRLNLAPATNYSLRVNC---ANRLGSP 298
QY      315 VADYIP 320
Db      299 XGDWVP 304

RESULT      5
GAD_RAT     STANDARD;      PRT;      449 AA.
AC      P18506;
DP      01-NOV-1990 (Rel. 16, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      GAMMA-AMINOBUTYRIC-ACID RECEPTOR DELTA SUBUNIT PRECURSOR (GABA(A)
DE      RECEPTOR).
GN      GABRD.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheta; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_Taxid=10116;
[1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=90380375; PubMed=2561970;
RA      Shivers B.D., Killisch I., Sprengel R., Sontheimer H., Koehler M.,
RA      Schofield P.R., Seeburg P.H.;
RT      "Two novel GABAA receptor subunits exist in distinct neuronal
RT      subpopulations."
RL      Neuron 3:327-337(1989).
[2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=90179746; PubMed=1690000;
RA      Zhao Z.Y., Joho R.H.;
RT      "Isolation of distantly related members in a multigene family using
RT      the polymerase chain reaction technique."
RL      Biochem. Biophys. Res. Commun. 167:174-182(1990).
[3]
RP      ERRATUM.
RA      Zhao Z.Y., Joho R.H.;
RC      Biochem. Biophys. Res. Commun. 168:887-887(1990).
-1- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
-1- VESTERARE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CHANNEL.
-1- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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EMBL; L08496; M4C42035.1; -.

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DR EMBL: M35162; AAA41182.1; -
 DR PIR: J00076; J00076.
 DR PIR: A34625; A34625.
 DR InterPro: IPR001188; -
 DR InterPro: IPR001175; -
 DR Pfam: PF00065; neur.chan.1.
 DR PRINTS: PRO0252; NR10NCHANNEL.
 DR PRINTS: PRO0253; GABAARRECEPT.
 DR PROSITE: PS00236; NEURON_ION_CHANNEL.1.
 DR Transmembrane.1.
 DR Transmembrane.1.
 FT SIGNAL 1 16
 FT CHAIN 17 449
 FT DOMAIN 17 248 GANMA-AMINO BUTYRIC-ACID RECEPTOR DELTA
 FT TRANSMEM 249 271 SUBUNIT.
 FT TRANSMEM 275 297 EXTRACELLULAR (PROBABLE).
 FT TRANSMEM 309 331 PROBABLE.
 FT DOMAIN 332 426 CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 427 449 PROBABLE.
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 164 178 BY SIMILARITY.
 SQ SEQUENCE 449 AA; 50566 MW; 64BDBCEB2C70AF CRC64;

Query Match 5.4%; Score 95; DB 1; Length 449;
 Best Local Similarity 22.2%; Pred. No. 1;

Matches 63; Conservative 44; Mismatches 85; Indels 92; Gaps 17;
 QY 16 LGWLLLLNLVLAAGRASPRLDPAPVCAQEGISCRVKN-----STCLDDSWI----- 63
 DB 4 LGWLL-----PLLT-----LCTQPHHGAARMADIGDYVSNLEISMLPLNDGL 47
 QY 64 ---HPKNLTP---SSPKNIYINLSYSTQHGELVPLVHFWLQTPASILLYGAEISYL 117
 DB 48 MEGARNRPRGIGGPPVVALLEVAIDH---ISEANNEYMTV---LHQSMROSRLS 101
 QY 118 QLTNTERLCVCFQFLSMLOHHRKRWRFSPHFVDPGQE--YEYVYH--LPRPIPDGPN 174
 DB 102 YNHNETIGLDSRFYDKL-----WLPDTFIVAKKSMFHDYVENKILRIQPDG--- 150
 QY 175 HSKIIIFVPCDESKMKMTTSCVSSGSLMDPNITVEYTLDTQHLRVDTLMNESPVOVL 234
 DB 151 ---VILY-----SIRITSTVAC-----DMDLAKYPMDEQECMLD-----L 182
 QY 235 ESFDSSEHSCFDVVKQIFAPROEEH-----QRANVTFTLSKF 273
 DB 183 ESY---GYSESDIV-YWSENEQIHLRLQLAQFTTSYRF 221

RESULT 6

GMCR_MOUSE STANDARD: PRT; 388 AA.
 AC 000941;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR RECEPTOR ALPHA
 DE CHAIN PRECURSOR (GM-CSF-R-ALPHA) (GMR).
 GN CSF2RA OR CSFGMA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Neonatal spleen;
 RX MEDLINE=92262426; PubMed=1533931;
 RA Park L.S., Martin U., Sorensen R., Luhr S., Morrissey P.J., Cosman D.,
 RA Larsen A.;
 RT "Cloning of the low-affinity murine granulocyte-macrophage colony-
 stimulating factor receptor and reconstruction of a high-affinity

RT receptor complex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4295-4299(1992).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
 CC FACTOR.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN
 CC IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE CYOKINE FAMILY OF RECEPTORS.
 CC
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DR EMBL: M85078; AAA37421.1; -
 DR MGI: MGI:1339754; Csf2ra.
 DR InterPro: IPR001777; -
 DR InterPro: IPR002996; -
 DR Pfam: PF00044; fn3.1.
 DR PROSITE: PS01356; HEMATOPO_REC_S_F2.1.
 DR Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 29
 FT CHAIN 30 388
 FT DOMAIN 30 327 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
 FT TRANSMEM 328 348 FACTOR RECEPTOR ALPHA CHAIN.
 FT TRANSMEM 349 388 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 43 43 INTRACELLULAR (POTENTIAL).
 FT CARBOHYD 43 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 388 AA; 41798 MW; 8C72E474360770FE CRC64;

Query Match 5.3%; Score 94; DB 1; Length 388;
 Best Local Similarity 21.6%; Pred. No. 1.1;

Matches 68; Conservative 35; Mismatches 108; Indels 104; Gaps 15;

QY 5 RCWPR-----VYGPALGWLILLNLVLAAGRASPRLDPAPVCAQEGIS 49
 DB 88 RCWPRRMALHGVTLVDYNGVGAAMHRLSFVESAAGCA-----ENIT 134
 QY 50 CRVNSTCLDDSWIHPKNLTPSPKNIYINLSV-SSTQH-----GELYVLHVEWT 99
 DB 135 CEIRAPARFLSCAM---REGPAAPADVRSLSRVLNSTGHDAVRCMADPDV---ITQC 186
 QY 100 LOTPASILYLGAEISYQLTNTNERLCYKF-----QFLSNL-----OHHRK 140
 DB 187 IANDLSL---GSEAYLVTVGRSGAGPVRFDDVATVATLRLGLGPRDVTASCNSSHCYV 243
 QY 141 RW-----RFSFHFVYDPGQE-----YEYVYHHLPRPIPDGPNHRSKII 180
 DB 244 SWAPRPTASLTARDPQGEVOMQSAEPGSTPRKYLVEETRLAFSPAHNG--GKHYKV- 300
 QY 181 FVPCDESKMKMTTSCVSSGSLMDPNITVEYTLDTQHLRVDTLMNESPVOVLSEFSDS 240
 DB 301 ---RAGDPRMK-----HWGEMSPAHNLEAEDT---RVPGALLVAVTACAVILLALAG 347
 QY 241 ENHSCFDVVKQIFAP 255
 DB 348 VTCRRFEVTRLRFP 362

RESULT 7

PF20_CHLRE STANDARD: PRT; 606 AA.
 ID PF20_CHLRE
 AC P93107;

DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE FLAGELLAR WD-REPEAT PROTEIN PF20.
 GN PF20.
 OS Chlamydomonas reinhardtii.
 CC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 CC Chlamydomonadales; Chlamydomonas.
 CC NCBI_TaxID=3055;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Smith E., Lefebvre P.;
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBUNIT: INTER-MICROTUBULE BRIDGES IN FLAGELLA.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 CC EMBL: U78547; AAB41727.1; -
 CC InterPro: IPR001680; -
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR PROSITE: PS00678; WD_REPEATS_1; 4.
 DR PROSITE: PS00682; WD_REPEATS_2; 6.
 DR PROSITE: PS0294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat; flagella.
 FT REPEAT 324 354 WD 1.
 FT REPEAT 366 396 WD 2.
 FT REPEAT 408 438 WD 3.
 FT REPEAT 450 480 WD 4.
 FT REPEAT 492 522 WD 5.
 FT REPEAT 534 564 WD 6.
 FT REPEAT 576 606 WD 7.
 SQ SEQUENCE 606 AA; 65839 MW; 7A8779501E321BD1 CRC64;

Query Match 5.1%; Score 89.5; DB 1; Length 606;
 Best Local Similarity 20.2%; Pred. No. 4.4;
 Matches 61; Conservative 34; Mismatches 118; Indels 89; Gaps 13;
 QY 10 VVPGALGWLILLNLVLAEGRASPRLL-LDPAPYCAQEGLSCRYKNSTCLDDSWIHPKNTL 68
 DB 283 VSAGPRSGW---ASLNAPRRNPYADLEPPAPVKMLSLKTFKGHL-----LSVANL 332
 QY 69 TPSSPKNIYINLSVSSST-----QHGEFLVPR--LHVEWTLQTD---ASILYLEGAEISY 116
 DB 333 ALHPTPLILTASDDKTWKWIMHFGDLIMCGEGHKWVAGVDHPAGTCLASGGGDSAV 392
 QY 117 LQNTNERLCVKEFOFLSMLOHNRKRMRFSHFVVDGQEEYEVNHLPKRIPDGDPRNHK 176
 DB 393 KIMDFEKORCV---TTFTHKQALWISVRF-----HHLGEVYVASSGLDHT 433
 QY 177 SKTIYVDCEDSKMKM-----TTSVSSGSLWDP----- 205
 DB 434 VRLMDLP---AGKCRVALRGHVDSVNDLAWOPFSSSLATASDKVSVWDAAGLCTQTY 490
 QY 206 -----NITVETLDIQHLRYD---FTLWNESTPYOV--LLESPFSDSEHNSCFPVYKQI 252
 DB 491 YGHONSCNGVSNILGIQLASTDADGVYKIMDTKMTAEVAITINCKHANKSCFPRSGV 550

RESULT 8
 YB79_YEAST

ID YB79_YEAST STANDARD; PRT; 954 AA.
 AC P38138;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PUTATIVE FAMILY 31 GLUCOSIDASE IN FAR2-BBP2 INTERGENIC REGION
 DE (EC 3.2.1.-).
 GN YBR296C OR YBR1526.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CC NCBI_TaxID=4932;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA STRAIN=S288C;
 RA Dubois E., el Bakoury M., Glansdorff N., Messenguy F., Pierard A.,
 RA Scherens B., Vierendeels F.;
 RL Submitted (AUG-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z36098; CAA85192.1; -
 CC PIR: S46105; S46105.
 CC SGI: S0000433; YBR229C.
 DR InterPro: IPR000322; -
 DR Pfam: PF01055; Glyco_hydro_31; 1.
 DR PROSITE: PS00129; GLYCOSYL_HYDROL_F31.1; 1.
 DR PROSITE: PS00707; GLYCOSYL_HYDROL_F31.2; FALSE_NEG.
 KW Hypothetical protein; Hydrolase; Glycosidase.
 FT ACT_SITE 537 537 BY SIMILARITY.
 SQ SEQUENCE 954 AA; 110265 MW; 92E93572F04FB009 CRC64;

Query Match 5.0%; Score 88.5; DB 1; Length 954;
 Best Local Similarity 22.4%; Pred. No. 9.3;
 Matches 67; Conservative 43; Mismatches 102; Indels 87; Gaps 18;
 QY 16 LCVLILLNLVLAEGRASPRLLDPAPYCAQEGLSCRYKNSTCLDDSWIHPKNTLPPSPKN 75
 DB 4 LKWLQQLVFF--AFSHAFDYLLKCAQSGFCHNR-----VYAEINIAKS--HH 50
 QY 76 IYINLSVSSSTQCELVYVAVENTLQTDASILYLEGAEISVQLQNTNERLCVKEFOFLSM 134
 DB 51 CYKKVDAESIANDPLENVLHAT--IKT--IPRIEGDIA-----VQPPESLSF 95
 QY 135 LQHH-----RKMRFSHFVVDGQEEYEVNHLPKRIPDGDPRNHKSKITFVDC 186
 DB 96 LODHSVFTINERKAPTNSGLISSQRENETWKVAFDKKQE-EANRIS---IQFH 150
 QY 187 DSKMKTTCVSSGSLMDP---NITVETLDIQHLR---VDTLWNESTPYOVL----- 234
 DB 151 ELKQKQTVN---SFWSKISSFLSLNSTADTFHLNAGDVSEIFAEE--PFOIKYWMON 203
 QY 235 -----ESFSDSEHNSCDFVYKQIFAPRQEEFHQANV-----TFTLSKFHNSCCHH 280
 DB 204 ALKLIYNEQNFLEIHH-----RTKQENP---AHVLPETTYNMRDNPLYSKH 249

RESULT 9
 GAD_HUMAN STANDARD; PRT; 452 AA.
 ID GAD_HUMAN
 AC 014764;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GAMMA-AMINOBUTYRIC-ACID RECEPTOR DELTA SUBUNIT PRECURSOR (GABA(A)

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DR EMBL; D26480; BAA05490.1; -
 DR EMBL; U02388; AAC50052.1; -
 DR EMBL; AB015306; BAA75823.1; -
 DR EMBL; AB015295; BAA75823.1; JOINED.
 DR EMBL; AB015296; BAA75823.1; JOINED.
 DR EMBL; AB015297; BAA75823.1; JOINED.
 DR EMBL; AB015298; BAA75823.1; JOINED.
 DR EMBL; AB015299; BAA75823.1; JOINED.
 DR EMBL; AB015300; BAA75823.1; JOINED.
 DR EMBL; AB015301; BAA75823.1; JOINED.
 DR EMBL; AB015302; BAA75823.1; JOINED.
 DR EMBL; AB015303; BAA75823.1; JOINED.
 DR EMBL; AB015304; BAA75823.1; JOINED.
 DR EMBL; AB015305; BAA75823.1; JOINED.
 DR EMBL; AC005336; AAC2730.1; -
 DR EMBL; AF221943; AAF86378.1; -
 DR MIM; 604426; -
 DR InterPro; IPR001128; -
 DR InterPro; IPR002402; -
 DR Pfam; PF00067; P450.1.
 DR PRINTS; PR00385; P450.
 DR PRINTS; PR00464; EP45011.
 DR PROSITE; PS00086; CYTOCHROME_P450.1.
 DR Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Microsome; Endoplasmic reticulum.
 FT BINDING 468 468
 FT CONFLICT 12 12 HEME (BY SIMILARITY).
 FT CONFLICT 12 13 W -> G (IN REF. 3).
 FT CONFLICT 12 13 WP -> CD (IN REF. 2).
 FT CONFLICT 12 13 WP -> CR (IN REF. 5).
 FT CONFLICT 336 333 GLSWYIYHIAKHPEYQER -> VSPGCTTLQSTQNTRSV
 FT CONFLICT 391 392 (IN REF. 2).
 FT CONFLICT 433 433 LH -> CI (IN REF. 2).
 FT CONFLICT 488 488 V -> M (IN REF. 3).
 FT CONFLICT 501 517 R -> A (IN REF. 2).
 FT CONFLICT 501 517 KPELVARAGGLWLRVE -> SRSWSCAQRADFGCGMS
 FT SEQUENCE 520 AA; 59853 MW; 1791F9EGECB59B5 CRC64;

Query Match 4.9%; Score 87; DB 1; Length 520;
 Best Local Similarity 20.0%; Pred. No. 5.9;
 Matches 61; Conservative 44; Mismatches 96; Indels 104; Gaps 18;

QY 60 DSKI-HPKNTLPPSPKNI---YINLVSSTQHGELVPYLVHVTLOTDSALILEGAE-L 114
 DB 142 DKWSRRHRRMLTPAFHNLILPKYKI-----FNESVINIMAKWQLASEGSACIDMFBI 195
 QY 115 SVYLQNTNRELCKVQFQF-----LSML---QHRRKRRRFSFSHEVVPVG 154
 DB 196 SLMTLDSLO-CV-FSDSDSCQEKRPSEYIAILELSALYSKRHHILHLIDLYLTLDG 253
 QY 155 QEV-----EYTVNHLPRIPDG-----DPNHSK-----IIFVPCDSKMK 191
 DB 254 QRRRACRLVHPTDAVIGRRRLTLPQGVDDFLQAKAKSKTLDFIDVLLSKDEGK-- 311
 QY 192 MTTSCVSSGSLMPNTVER-----LDIQHLAVDTLWV-ESTPVOVLESTSDSEN 242
 DB 312 -----KLSDEDIKRAEDTFMEGHDTTASGLSWLYLHAKHPEYQ----- 351
 QY 243 HSGEDVYKQIFARQEEFHQRANVTFLSKFHMCCHNHVQCFPFSSCLNCLRHAVTP 302
 DB 352 ERKROEYDLELKDREK-----ELEWDLAHL--PFLTMCKESLR--LHP 394
 QY 303 CPVYS 307

DB 395 VPVYS 399

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RESULT 11
 TUD_DROME
 ID TUD_DROME STANDARD: PRT; 2515 AA.
 AC P25823;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE MATERNAL TUDOR PROTEIN.
 GN TUD.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92038995; PubMed=1936993;
 RA Golubieski G.S., Bardsley A., Tax F., Boswell R.E.;
 RT "Tudor, a posterior-group gene of Drosophila melanogaster, encodes a
 novel protein and an mRNA localized during mid-oogenesis";
 RL Genes Dev. 5:2060-2070(1991).
 CC -1- FUNCTION: REQUIRED DURING OOGENESIS FOR THE FORMATION OF
 PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.
 CC -1- MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR
 REGION OF THE DEVELOPING OOCYTE DURING THE EARLY TO MIDDLE STAGES
 OF OOOGENESIS.

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DR EMBL; X62420; CAA44286.1; -
 DR PIR; A41519; A41519.
 DR Flybase; FBgn003891; tud.
 DR InterPro; IPR001097; -
 DR Pfam; PF00567; TUDOR; 10.
 KW Developmental protein.
 FT SEQUENCE 2515 AA; 285236 MW; 683C100AD308BADA CRC64;

Query Match 4.9%; Score 87; DB 1; Length 2515;
 Best Local Similarity 22.6%; Pred. No. 41;
 Matches 77; Conservative 50; Mismatches 119; Indels 94; Gaps 20;

QY 58 LDDSWHPRKNTPS-----SPKNTYINLVSSTQHGELVPYLVHVTLOTDSALIL 107
 DB 1003 LDKPYALQEKTPSKKAASLSWLSPPQFYTPKVSATKDNTKDMR-EFYRKQKQPL 1061
 QY 108 YLE-GAELSVLQNTNRELCKVQFQFSLMLQHNRRKRRFSFSHEVVPVGQDEYVT--VHH 163
 DB 1062 QLKVGSTVYVVRQKDAILRAT---VTACNHMMRKRYV---FCVDIGSLITVTSEDIWQ 1114
 QY 164 LKRPIDG-----DPNHSKITI---FVP-----DCE-DSKKK----- 191
 DB 1115 LEQRFADPPCMARHRCSEFHSVYTNVDPY---IVDRMETFVPVNAKYDCEVSKESNQS 1171
 QY 192 -MTSC-----VSSGSLMD-----PNITVEFLDQHLVVDFTLWNESTPYQ 231
 DB 1172 MTSSTSYVNIIFVNGASLDMLVKAELLTEVAPETIRVNLAAQQIGKFTSIDMTSFK 1231
 QY 232 VLESEFSDESEHSC-FDVYKQI-----FAPROEFHORANVTFLSKFHMCCHNHVQCF 285
 DB 1232 VQPD-YGNVNVFLCTYDDAKAFVANSPLARPKFEYE--GKSFLANVKVNCENNIVHLRP 1288

QY 286 FFSSCLNDCLRHAVTPCPVISNT-----TVPKPVADYI 319
DB 1289 VMPLMED--RRSFICPPYVLSSFOALVVTAKPRVYV 1326

RESULT 12
ID ICE4_HUMAN STANDARD; PRT; 377 AA.
AC P49662;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CASPASE-4 PRECURSOR (EC 3.4.22.-) (CASP-4) (ICH-2 PROTEASE) (TX
DE PROTEASE) (ICE/REL-11).
GN CASP4 OR ICH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., MUTAGENESIS OF C-258, AND 3D-STRUCTURE MODELING.
RC TISSUE=Placenta;
RX MEDLINE=95262631; PubMed=7743998;
RA Feucheu C., Diu A., Chan A.W.E., Blanchet A.-M., Miossec C., Heve F.,
RA Colliard-Butlleil V., Gu Y., Aldape R.A., Lippe J.A., Kocher C.,
RA Su M.S.-S., Livingston D.J., Hercend T., Lalanne J.-L.;
RA "A novel human protease similar to the interleukin-1 beta converting
RT enzyme induces apoptosis in transfected cells.";
RL EMO J. 14:1914-1922(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95318183; PubMed=7797592;
RA Munday N.A., Vaillancourt J.P., Ali A., Casano F.J., Miller D.K.,
RA Molineaux S.M., Yaman T.T., Yu V.L., Nicholson D.W.;
RA "Molecular cloning and pro-apoptotic activity of ICErelIII and
RT ICErelIII, members of the ICE/CED-3 family of cysteine proteases.";
RL J. Biol. Chem. 270:15870-15876(1995).
RN [3]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Thymus;
RX MEDLINE=95318091; PubMed=7797510;
RA Ramens J., Paskind M., Hugunin M., Talarian R.V., Allen H., Banach D.,
RA Bump N.J., Hackett M.C., Johnston C.G., Li P., Manovich J.A.,
RA Teranova M., Ghayur T.;
RA "Identification and characterization of ICH-2, a novel member of the
RT interleukin-1 beta-converting enzyme family of cysteine proteases.";
RL J. Biol. Chem. 270:15250-15256(1995).
RN [4]
RP FUNCTION. INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES CASPASE-1.
CC SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY
CC SIMILARITY).
CC TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN
CC SPLEEN AND LUNG. MODERATE EXPRESSION IN HEART AND LIVER, LOW
CC EXPRESSION IN SKELETAL MUSCLE, KIDNEY AND TESTIS. NOT FOUND IN THE
CC BRAIN.
CC -1- PTM: THE TWO SUBUNITS ARE DERIVED FROM THE PRECURSOR SEQUENCE BY
CC AN AUTOCATALYTIC MECHANISM OR BY CLEAVAGE BY CASPASE-8.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14; ALSO KNOWN AS THE
CC CASPASE FAMILY.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- CAUTION: THIS PROTEIN COULD BE THE HUMAN ORTHOLOG OF MOUSE
CC CASPASE-11.
CC -----
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CC -----
CC EMBL; Z48810; CAAB8750.1; -;
DR EMBL; U28014; AAA75171.1; -;

DR EMBL; U28804; AAA86890.1; -;
DR HSSP; P29466; IIBC.
DR MEROPS; C14.007; -;
DR MIM; 602664; -;
DR InterPro; IPR001309; -;
DR InterPro; IPR001315; -;
DR InterPro; IPR002138; -;
DR InterPro; IPR002398; -;
DR Pfam; PF00619; CARD. 1.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILIBCENZME.
DR PROSITE; PS50209; CARD. 1.
DR PROSITE; PS01122; CASPASE_CYS. 1.
DR PROSITE; PS01121; CASPASE_HIS. 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 780
FT CHAIN 781 270
FT PROPEP 271 289
FT CHAIN 290 377
FT DOMAIN 6 81
FT ACT_SITE 210 210
FT ACT_SITE 258 258
FT MTAGEN 258 258
SQ SEQUENCE 377 AA; 43362 MW; DC7CC6B9D483EB CRC64;
C->S: LOSS OF ACTIVITY.

Query Match 4.9%; Score 86.5; DB 1; Length 377;
Best Local Similarity 24.6%; Pred. No. 4.4;
Matches 29; Conservative 13; Mismatches 33; Indels 43; Gaps 6;

QY 176 KSKIIFPDCCDSKMKMTSCVSSGLW--DPNIVETLDIQ-----HLRVD 220
DB 249 KPKIIVQACGGA-----NRGELWROSPALFVASSOSSENLDEADYKTHVEAD 299
QY 221 FTLWNESTPYOVLESFSDSENHSCFDVVKQIFAPROEFHORANVFTLSKFMWCH 278
DB 300 FIACSSPHNV-----SWRDSITGSIFF--ITQLIT-----CFQKYSWMCCH 338

RESULT 13
LMA3_MOUSE STANDARD; PRT; 2569 AA.
ID LMA3_MOUSE 061789; 061966;
AC 061789; 061788; 061966;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LAMININ ALPHA-3 CHAIN PRECURSOR (FRAGMENT).
GN LMA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Lung;
RX MEDLINE=95394948; PubMed=7665604;
RA Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Meneguzzi G.;
RA "Cloning and complete primary structure of the mouse laminin alpha 3
RT chain. Distinct expression pattern of the laminin alpha 3a and alpha
RT 3b chain isoforms.";
RL J. Biol. Chem. 270:21820-21826(1995).
RN [2]
RP REVISIONS.
RA Aberdam D.;
RN Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1052-1770 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94281750; PubMed=8012114;
RA Aberdam D., Galliano M.-F., Mattei M.-G., Pisani-Spadafora A.,

Query Match 4.9%; Score 86; DB 1; Length 2569;
 Best Local Similarity 20.9%; Pred. No. 51; Mismatches 66; Gaps 12;
 Matches 56; Conservative 41; Indels 113; Indels 66; Gaps 12;

CC 28 PGRASPLLDPPA-PCVAC-EGISCRV-----KNSTCLDSDMHP-KMLTSSPKNIYI 78
 CC 1780 PGFELPRLRPPKGCIGLIDLNLNENLVNFKTTENLNTVEVECRKRKESDKNYFE 1839
 CC 79 NLAVSTQHGVLVPLVHVEWLTQ--DASILYLEGAEISVLOLNTNE-RLCVKQ----- 130
 CC 1840 GTGYARIPTOPNAPFPKLSMTIQTVDRLGLFEAFENODNFISLINEDGNLMVYKINSEP 1899
 CC 131 -----FLSMQHHKRRKRRSEFS-HFVYDPCOEYEVYVHNL---EKPIP 169
 CC 1900 PKEGIDTINNGRDHMLLISGSQKMLNMNKHSHIIEGIDFESTYVYLGIPAIR 1959
 CC 170 DGDG-----NHSKRIIFVPD-----CEDSKMKMTSCVSSGSLMPNIT 208
 CC 1960 ERFPLSTPAFGCKMNLKKTSGVRLNDTVGVTCKCEDMKLVRTASFSRGQGMSTNLD 2019
 CC 209 VETIDTQHLRVD-----TLVNESTPYOVLSESD 239
 CC 2020 VPSLDRQLSPGFQTFQPSGTLNHNQRTSSLLVTLIED 2057

RESULT 14
 DP3A_VIBCH STANDARD; PRT; 1164 AA.

ID DP3A_VIBCH STANDARD; PRT; 1164 AA.
 AC P52022; Q9KPM7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7).
 GN DNAE OR VC2245.
 OS *Vibrio cholerae*.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR INABA C6706 / SEROTYPE O1;
 RX MEDLINE=97074686; PubMed=8917113;
 RA Franco A.A., Yeh P.E., Johnson J.A., Barry E.M., Guerra H., Maurer R., Morris J.G., Jr.,
 RA "Cloning and characterization of dnaE, encoding the catalytic subunit of replicative DNA polymerase III, from *Vibrio cholerae* strain C6706.";
 RA Gene 175:281-283(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unaym L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback L., Fleischmann R.D., Mermin W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
 RA "DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.";
 RL Nature 406:477-483(2000).
 CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTISUBUNIT ENZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY. THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE + DNA(N).
 CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA CHAINS) THAT CAN REPAIR SHORT GAPS CREATED BY NUCLEASE IN DUPLICATION. FOR EFFICIENT REPLICATION OF THE LONG, SINGLE-STRANDED TEMPLATES, POL III REQUIRES THE AUXILIARY CHAINS BETA, GAMMA, AND DELTA (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

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 CC -----
 CC EMBL: U30472; AAC44578.1; ALT_INIT.
 CC EMBL: AE004296; AAF95389.1; -.
 DR TIGR: VC2245; -.
 DR TRANSFERASE, DNA-directed DNA polymerase; DNA replication.
 KM TRANSFERASE, DNA-directed DNA polymerase; DNA replication.
 FT CONFLICT 348 348 I->V (IN REF. 1).
 FT CONFLICT 485 487 ALQ->ELK (IN REF. 1).
 FT CONFLICT 685 685 T->P (IN REF. 1).
 FT CONFLICT 1000 1000 V->A (IN REF. 1).
 FT CONFLICT 1030 1030 M->L (IN REF. 1).
 FT CONFLICT 1103 1103 E->G (IN REF. 1).
 FT CONFLICT 1117 1117 V->A (IN REF. 1).
 SQ SEQUENCE 1164 AA; 130604 MW; EDAFE70BB830F293 CRC64;

Query Match 4.8%; Score 85.5; DB 1; Length 1164;
 Best Local Similarity 19.9%; Pred. No. 21; Mismatches 91; Indels 111; Gaps 15;
 Matches 61; Conservative 44; Mismatches 91; Indels 111; Gaps 15;

CC 21 LILNVLPAGRASPLLDPPAPVCAOGL-----SCRVK----- 53
 CC 32 LVKVAAMGMAMALTDI-TNLC---GLVKFSTAHNGCYKRIIGADFTLOSSEFDELT 87
 CC 54 NSTCLDSDMHPKMLTPSSPKNIYINLSVSTQ---HGEVLVPLVHVEWLTQDASILYLE 110
 CC 88 KLTLLAKNNVGYKNLT-----LISKAYLNGHVQGVVIDKAMVVENAEGILVLS 137
 CC 111 G---AELSVLOLNTNER---LCVKQ-----FLSMQHHKRRKRRSEFSHPVDPGE 156
 CC 138 GKSGEGRALKNGQOQVERCIEFYQTHFADHFLYELRLTRRAD-EESYLHFDLDAVQ 196
 CC 157 YEYVHHLPRIPDPPHKSRIIFVPPCEDSKMKMTSCVSSGSLMDPNIVETLDTQH 216
 CC 197 YDLPV-----VATNEVF-----LTESFEANE 219
 CC 217 LRV---DEFLMNESTPYOVLSEFSDENSHSCFDVVKOIFAPROE-----EFHORAV 266
 CC 220 IRVAILHDGYTLEDDRRPRKNYSPKQYLRSEAEWC-----ELFADIDEALANSVEIARCV 274
 CC 267 TETLSKF 273
 CC 275 TVRLGEY 281

RESULT 15
 DBL_HUMAN STANDARD; PRT; 925 AA.
 ID DBL_HUMAN STANDARD; PRT; 925 AA.
 AC P10911; P14919;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PROTO-ONCOGENE DBL PRECURSOR [CONTAINS: MCF2].
 GN DBL OR MCF2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=89052660; PubMed=3056717;
 RA Ron D., Tronick S.R., Aaronson S.A., Eva A.;
 RA "Molecular cloning and characterization of the human db1 proto-oncogene: evidence that its overexpression is sufficient to transform NIH/3T3 cells";

RL EMBO J. 7:2465-2473(1988).
 RN REVISIONS.
 RP Ron D.;
 RL Submitted (JUN-1989) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 498-925 FROM N.A.
 RX MEDLINE=88176886; PubMed=3281159;
 RA Eva A., Vecchio G., Rao C.D., Tronick S.R., Aaronson S.A.;
 RT "The predicted DBL oncogene product defines a distinct class of
 RT transforming proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2061-2065(1988).
 RN [4]
 RP SEQUENCE OF 398-925 FROM N.A.
 RX MEDLINE=94167115; PubMed=2577874;
 RA Nouguchi T., Gailand F., Batcz M., Mattei M.-G., Birnbaum D.;
 RT "Activation of a mcf.2 oncogene by deletion of amino-terminal coding
 RT sequences.";
 RL Oncogene 3:709-715(1988).
 RN [5]
 RP DBL-HOMOLOGY DOMAIN, AND MUTAGENESIS.
 RX MEDLINE=91591759; PubMed=2065022;
 RA Ron D., Zannini M., Lewis M., Wickner R.B., Hunt L.T., Graziani G.,
 RT Tronick S.R., Aaronson S.A., Eva A.;
 RT "A region of proto-dbl essential for its transforming activity shows
 RT sequence similarity to a yeast cell cycle gene, CDC24, and the human
 RT breakpoint cluster gene, bcr.";
 RL New Biol. 3:372-379(1991).
 RN [6]
 RP CHARACTERIZATION OF DBL DOMAIN.
 RX MEDLINE=94103281; PubMed=8276860;
 RA Hart M.J., Eva A., Zangrilli D., Aaronson S.A., Evans T.,
 RT Cerione R.A., Zheng Y.;
 RT "Cellular transformation and guanine nucleotide exchange activity are
 RT catalyzed by a common domain on the dbl oncogene product.";
 RL J. Biol. Chem. 269:62-65(1994).
 RN -1- FUNCTION: PROMOTES THE EXCHANGE OF G25K-BOUND GDP BY GTP. ACTS AS
 RN A GUANINE NUCLEOTIDE EXCHANGE FACTOR FOR CDC42 AND RHOA, BUT NOT
 RN FOR RAC1 AND TC10. CAN BE ACTIVATED BY TRUNCATION OF THE N-
 RN TERMINUS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL BRAIN AND ADRENAL GLANDS;
 CC IN THE ADULT, EXPRESSION IS LIMITED TO TESTES, OVARIES AND BRAIN.
 CC -1- DOMAIN: THE DBL DOMAIN IS ESSENTIAL FOR TRANSFORMING ACTIVITY AND
 CC DIRECTLY CATALYZES GDP-GTP EXCHANGE ACTIVITY.
 CC -1- DISASE: MCF.2 AND DBL REPRESENT TWO ACTIVATED VERSIONS OF THE
 CC SAME PROTO-ONCOGENE.
 CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X12556; CAA31069.1; .
 DR EMBL: J03639; AAA52172.1; ALT_INIT.
 DR EMBL: X13230; CAA31617.1; ALT_SEQ.
 DR PIR: A30040; TVHUBD.
 DR PIR: A28051; TVHUBD.
 DR MIM: 311030; .
 DR InterPro: IPR000219; .
 DR InterPro: IPR000947; .
 DR InterPro: IPR001331; .
 DR InterPro: IPR001849; .
 DR Pfam: PR00169; PH.1.
 DR Pfam: PR00621; RHOGEF.1.
 DR PRINTS: PR00615; CCAATSUBUNTA.
 DR PROSITE: PS00741; GDS_CDC24; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.

KW Guanine-nucleotide releasing factor; Proto-oncogene; Phosphorylation;
 KM Transforming protein.
 FT CHAIN 398 925
 FT CHAIN 498 925 MCF2 TRANSFORMING PROTEIN.
 FT CHAIN 498 925 DBL TRANSFORMING PROTEIN.
 FT DOMAIN 498 686 DH.
 FT DOMAIN 687 809 PH.
 FT MOD_RES 742 742 PHOSPHORYLATION.
 FT MUTAGEN 640 646 LKELL->IIRDTI: TRANSFORMATION
 FT CAPABILITY REDUCED; NO STIMULATION OF GDP
 FT DISSOCIATION.
 FT R -> Q (IN REF. 4).
 FT A -> V (IN REF. 3).
 FT SEQUENCE 925 AA; 107657 MW; 0BCB303276D19C9 CRC64;
 SQ
 Query Match 4.8%; Score 85; DB 1; Length 925;
 Best Local Similarity 25.2%; Pred. No. 18;
 Matches 33; Conservative 22; Mismatches 58; Indels 18; Gaps 4;
 QY 178 KIIFFPDCEDSKMKMTTSCVSSGSLMD--PNITVETLDQHLRVDFTLNNESTPYOVL 234
 DB 467 KIEVFPDQCKRSGSSSSLDNGNSLDVLRKNHVNELIQTERTYV-----RELITVLL 519
 QY 235 ESEFSEENSHSCFDPV-----KQIFAPROEFHORANVTFTLSKFFWCCHHHVQVOPFF 287
 DB 520 GYRAENDNPENMFDPMLPLLNKKDILFGNMAETIYEFNDIF-LSLENCAPAPRVGCF 578
 QY 288 SSGLDNCLRHA 298
 DB 579 LERRKDFQMA 589

Search completed: July 17, 2001, 11:21:04
 Job time: 158 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 17, 2001, 11:16:31 ; Search time 21.86 seconds
(without alignments)
296.733 Million cell updates/sec

Title: US-09-488-728-2_COPY_1_322
Perfect score: 1766
Sequence: 1 MAIRRCMPRVDPGALGWL.....CPVISNTVPKPVADYIPLW 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1766	100.0	864	2	US-08-620-694A-2
2	1766	100.0	864	3	US-09-022-255-2
3	1766	100.0	864	3	US-09-022-636-2
4	1766	100.0	864	3	US-08-978-773-2
5	1766	100.0	864	3	US-09-022-253-2
6	1766	100.0	864	3	US-09-022-260-2
7	1766	100.0	864	4	US-09-022-259-2
8	1766	100.0	864	4	US-09-022-257-2
9	1254	71.0	866	2	US-08-620-694A-10
10	1254	71.0	866	3	US-09-022-255-10
11	1254	71.0	866	3	US-09-022-696-10
12	1254	71.0	866	3	US-08-978-773-4
13	1254	71.0	866	3	US-09-022-253-10
14	1254	71.0	866	3	US-09-022-260-10
15	1254	71.0	866	4	US-09-022-259-10
16	1254	71.0	866	4	US-09-022-257-10
17	97.5	5.5	379	4	US-08-908-436-5
18	97	5.5	880	1	US-08-445-640-10
19	97	5.5	880	3	US-08-170-558-10
20	97	5.5	880	3	US-08-447-314-10
21	97	5.5	880	3	US-08-445-661-10
22	88	5.0	874	2	US-08-456-647B-6
23	88	5.0	874	2	US-08-237-401A-6
24	86.5	4.9	377	3	US-08-776-900C-2
25	86.5	4.9	377	3	US-08-721-986-9
26	86.5	4.9	377	4	US-08-225-487A-9
27	86.5	4.9	377	4	US-09-268-195C-2

28	86.5	4.9	377	5	PCT-US94-07127A-2	Sequence 2, Appl1
29	86.5	4.9	377	5	PCT-US96-10521-12	Sequence 12, Appl1
30	83.5	4.7	1213	1	US-08-188-582-20	Sequence 20, Appl1
31	83.5	4.7	1213	1	US-08-646-715-20	Sequence 20, Appl1
32	82.5	4.7	333	1	US-08-436-463-6	Sequence 6, Appl1
33	82.5	4.7	333	1	US-08-024-253-6	Sequence 6, Appl1
34	81.5	4.6	1153	1	US-08-173-497-3	Sequence 3, Appl1
35	81.5	4.6	1153	1	US-08-286-889-3	Sequence 3, Appl1
36	81.5	4.6	1153	1	US-08-485-618-3	Sequence 3, Appl1
37	81.5	4.6	1153	1	US-08-362-652-3	Sequence 3, Appl1
38	81.5	4.6	1153	2	US-08-605-672-3	Sequence 3, Appl1
39	81.5	4.6	1153	2	US-08-402-293A-3	Sequence 3, Appl1
40	81.5	4.6	1153	2	US-08-943-353-3	Sequence 3, Appl1
41	81	4.6	553	3	US-08-630-172-13	Sequence 13, Appl1
42	81	4.6	839	1	US-08-087-016-2	Sequence 2, Appl1
43	81	4.6	2813	3	US-08-896-449A-2	Sequence 2, Appl1
44	81	4.6	2813	3	US-09-132-652-2	Sequence 2, Appl1
45	79.5	4.5	364	1	US-08-680-726A-56	Sequence 56, Appl1

ALIGNMENTS

RESULT 1
US-08-620-694A-2
; Sequence 2, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-620-694A-2

Query Match 100.0%; Score 1766; DB 2; Length 864;
Best Local Similarity 100.0%; Pred. No. 1,1e-183;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAIRRCMPRVVPGPALGMLLLNLNVLAPGRASPRLLDFPAPVCAQEGLSGRVKNSTCLDD 60
1 MAIRRCMPRVVPGPALGMLLLNLNVLAPGRASPRLLDFPAPVCAQEGLSGRVKNSTCLDD 60
61 SWIHPKNTLPSSPKNIYINLSVSTQHGELVPLVHVEWTLQTDASTLYEGAEISVQLN 120
61 SWIHPKNTLPSSPKNIYINLSVSTQHGELVPLVHVEWTLQTDASTLYEGAEISVQLN 120
121 TNERLCVAFQFLSMLOHHKRRMFSESHFVVDPGQEVTVHHLPKPIPDGDPNHSKII 180
121 TNERLCVAFQFLSMLOHHKRRMFSESHFVVDPGQEVTVHHLPKPIPDGDPNHSKII 180
181 FVPDCEDSKMKWTSCVSSGSLMDPNITVETLDTQHLRVDFTLMNSTPYQVLLSEFSDS 240
181 FVPDCEDSKMKWTSCVSSGSLMDPNITVETLDTQHLRVDFTLMNSTPYQVLLSEFSDS 240
241 ENHSCFDVVKQIFAPROEFHORANVTFTLSKFFHMCCHHVQVQPFSSCLNDCLRHAVT 300
241 ENHSCFDVVKQIFAPROEFHORANVTFTLSKFFHMCCHHVQVQPFSSCLNDCLRHAVT 300
301 VPCPVISNTVTPKPVADYIPLW 322
301 VPCPVISNTVTPKPVADYIPLW 322

RESULT 2
US-09-022-255-2
Sequence 2, Application US/09022255
Patent No. 6072033

GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-2

Query Match 100.0%; Score 1766; DB 3; Length 864;
Best Local Similarity 100.0%; Pred. No. 1,1e-183;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAIRRCMPRVVPGPALGMLLLNLNVLAPGRASPRLLDFPAPVCAQEGLSGRVKNSTCLDD 60
1 MAIRRCMPRVVPGPALGMLLLNLNVLAPGRASPRLLDFPAPVCAQEGLSGRVKNSTCLDD 60
61 SWIHPKNTLPSSPKNIYINLSVSTQHGELVPLVHVEWTLQTDASTLYEGAEISVQLN 120
61 SWIHPKNTLPSSPKNIYINLSVSTQHGELVPLVHVEWTLQTDASTLYEGAEISVQLN 120
121 TNERLCVAFQFLSMLOHHKRRMFSESHFVVDPGQEVTVHHLPKPIPDGDPNHSKII 180
121 TNERLCVAFQFLSMLOHHKRRMFSESHFVVDPGQEVTVHHLPKPIPDGDPNHSKII 180
181 FVPDCEDSKMKWTSCVSSGSLMDPNITVETLDTQHLRVDFTLMNSTPYQVLLSEFSDS 240
181 FVPDCEDSKMKWTSCVSSGSLMDPNITVETLDTQHLRVDFTLMNSTPYQVLLSEFSDS 240
241 ENHSCFDVVKQIFAPROEFHORANVTFTLSKFFHMCCHHVQVQPFSSCLNDCLRHAVT 300
241 ENHSCFDVVKQIFAPROEFHORANVTFTLSKFFHMCCHHVQVQPFSSCLNDCLRHAVT 300
301 VPCPVISNTVTPKPVADYIPLW 322
301 VPCPVISNTVTPKPVADYIPLW 322

RESULT 3
US-09-022-696-2
Sequence 2, Application US/09022696
Patent No. 6072037

GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-696-2

Query Match 100.0%; Score 1766; DB 3; Length 864;
Best Local Similarity 100.0%; Pred. No. 1,1e-183;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIRCPRRVVPGRALGMLLLNLVLAAGRASPRLDPPAPCAOEGISCRVKNSTCLDD 60
DB 1 MAIRCPRRVVPGRALGMLLLNLVLAAGRASPRLDPPAPCAOEGISCRVKNSTCLDD 60
QY 61 SWIRKMLTPSSPKNIYINLSVSTOGHELVPVLAHVEMTLQTDASILYLEGAEISVLQIN 120
DB 61 SWIRKMLTPSSPKNIYINLSVSTOGHELVPVLAHVEMTLQTDASILYLEGAEISVLQIN 120
QY 121 TNERLCYKFOFLSMLOHRRKRMRESFSHFVVDPGQEEYEVTVHLLPKPIPDGDPNHSKII 180
DB 121 TNERLCYKFOFLSMLOHRRKRMRESFSHFVVDPGQEEYEVTVHLLPKPIPDGDPNHSKII 180
QY 181 FVPCEDESKMKMTTSCVSSGSLMDPNITVEITLDIOLKRVDFLNMESTPYQVLLSEFSDS 240
DB 181 FVPCEDESKMKMTTSCVSSGSLMDPNITVEITLDIOLKRVDFLNMESTPYQVLLSEFSDS 240
QY 241 ENHSCFVVKOIFAPROBEFHORANVTFTLSKFHWCCHHHVOVOFFSSCLNDCLRHAAT 300
DB 241 ENHSCFVVKOIFAPROBEFHORANVTFTLSKFHWCCHHHVOVOFFSSCLNDCLRHAAT 300
QY 301 VPCPVISNTTVKRPVADYIPLM 322
DB 301 VPCPVISNTTVKRPVADYIPLM 322

RESULT 4
US-08-978-773-2

; Sequence 2, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Froult, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,773
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/052,525
; FILING DATE: 27 NOVEMBER 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2623-A

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-773-2

Query Match 100.0%; Score 1766; DB 3; Length 864;
Best Local Similarity 100.0%; Pred. No. 1,1e-183;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIRCPRRVVPGRALGMLLLNLVLAAGRASPRLDPPAPCAOEGISCRVKNSTCLDD 60
DB 1 MAIRCPRRVVPGRALGMLLLNLVLAAGRASPRLDPPAPCAOEGISCRVKNSTCLDD 60
QY 61 SWIRKMLTPSSPKNIYINLSVSTOGHELVPVLAHVEMTLQTDASILYLEGAEISVLQIN 120
DB 61 SWIRKMLTPSSPKNIYINLSVSTOGHELVPVLAHVEMTLQTDASILYLEGAEISVLQIN 120
QY 121 TNERLCYKFOFLSMLOHRRKRMRESFSHFVVDPGQEEYEVTVHLLPKPIPDGDPNHSKII 180
DB 121 TNERLCYKFOFLSMLOHRRKRMRESFSHFVVDPGQEEYEVTVHLLPKPIPDGDPNHSKII 180
QY 181 FVPCEDESKMKMTTSCVSSGSLMDPNITVEITLDIOLKRVDFLNMESTPYQVLLSEFSDS 240
DB 181 FVPCEDESKMKMTTSCVSSGSLMDPNITVEITLDIOLKRVDFLNMESTPYQVLLSEFSDS 240
QY 241 ENHSCFVVKOIFAPROBEFHORANVTFTLSKFHWCCHHHVOVOFFSSCLNDCLRHAAT 300
DB 241 ENHSCFVVKOIFAPROBEFHORANVTFTLSKFHWCCHHHVOVOFFSSCLNDCLRHAAT 300
QY 301 VPCPVISNTTVKRPVADYIPLM 322
DB 301 VPCPVISNTTVKRPVADYIPLM 322

RESULT 5
US-09-022-253-2

; Sequence 2, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Sprigow, Melanie
; TITLE OF INVENTION: NO. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-253-2

Query Match 100.0%; Score 1766; DB 3; Length 864;
Best Local Similarity 100.0%; Pred. No. 1.le-183;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIRRCWPRVVGPRALGWLILLNLVLAAPGRASPRLLDFPAPVCAOGLSCRYKNSCTCLDD 60
DB 1 MAIRRCWPRVVGPRALGWLILLNLVLAAPGRASPRLLDFPAPVCAOGLSCRYKNSCTCLDD 60
QY 61 SWIHRKNLPPSSPKNIYINLVSSTOHELVPYLHVEWTLQTDASIIYLEGAEISVQLN 120
DB 61 SWIHRKNLPPSSPKNIYINLVSSTOHELVPYLHVEWTLQTDASIIYLEGAEISVQLN 120
QY 121 TNERLCVKQFQLSMLOHHRKRMFSFHFVVDGQEVYVHHLPRIPDGPNNHKSII 180
DB 121 TNERLCVKQFQLSMLOHHRKRMFSFHFVVDGQEVYVHHLPRIPDGPNNHKSII 180
QY 181 FVPDCEDESKMKTTSCVSSGSLMDPNITVETLDTQHLRVDFTLMNSTPYQVLLSEFSDS 240
DB 181 FVPDCEDESKMKTTSCVSSGSLMDPNITVETLDTQHLRVDFTLMNSTPYQVLLSEFSDS 240
QY 241 EHNHSCFDVVKQIFAPRQEFHQRANVTFTLSKPFHWCCHHHVQVQPFSSCLNDCLRAHVT 300
DB 241 EHNHSCFDVVKQIFAPRQEFHQRANVTFTLSKPFHWCCHHHVQVQPFSSCLNDCLRAHVT 300
QY 301 VPCPVISNTTVPKPVADYIPLW 322
DB 301 VPCPVISNTTVPKPVADYIPLW 322

RESULT 6
US-09-022-260-2
Sequence 2, Application US/09022260
Patent No. 6100235
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-260-2

Query Match 100.0%; Score 1766; DB 3; Length 864;
Best Local Similarity 100.0%; Pred. No. 1.le-183;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIRRCWPRVVGPRALGWLILLNLVLAAPGRASPRLLDFPAPVCAOGLSCRYKNSCTCLDD 60
DB 1 MAIRRCWPRVVGPRALGWLILLNLVLAAPGRASPRLLDFPAPVCAOGLSCRYKNSCTCLDD 60
QY 61 SWIHRKNLPPSSPKNIYINLVSSTOHELVPYLHVEWTLQTDASIIYLEGAEISVQLN 120
DB 61 SWIHRKNLPPSSPKNIYINLVSSTOHELVPYLHVEWTLQTDASIIYLEGAEISVQLN 120
QY 121 TNERLCVKQFQLSMLOHHRKRMFSFHFVVDGQEVYVHHLPRIPDGPNNHKSII 180
DB 121 TNERLCVKQFQLSMLOHHRKRMFSFHFVVDGQEVYVHHLPRIPDGPNNHKSII 180
QY 181 FVPDCEDESKMKTTSCVSSGSLMDPNITVETLDTQHLRVDFTLMNSTPYQVLLSEFSDS 240
DB 181 FVPDCEDESKMKTTSCVSSGSLMDPNITVETLDTQHLRVDFTLMNSTPYQVLLSEFSDS 240
QY 241 EHNHSCFDVVKQIFAPRQEFHQRANVTFTLSKPFHWCCHHHVQVQPFSSCLNDCLRAHVT 300
DB 241 EHNHSCFDVVKQIFAPRQEFHQRANVTFTLSKPFHWCCHHHVQVQPFSSCLNDCLRAHVT 300
QY 301 VPCPVISNTTVPKPVADYIPLW 322
DB 301 VPCPVISNTTVPKPVADYIPLW 322

RESULT 7
US-09-022-259-2
Sequence 2, Application US/09022259
Patent No. 6191104
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022.259
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-259-2

Query Match 100.0%; Score 1766; DB 4; Length 864;
Best Local Similarity 100.0%; Pred. No. 1,1e-183;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIRRCPRVVPGALGMLLLNLVLAAGRASPRLDPAPVCAOEGISCRVKNSTCLDD 60
DB 1 MAIRRCPRVVPGALGMLLLNLVLAAGRASPRLDPAPVCAOEGISCRVKNSTCLDD 60
QY 61 SWIHPKMLTPSSPNITINLSVSSQHGELVPVLAHEWTLQTDASILYLEGALSVLQLN 120
DB 61 SWIHPKMLTPSSPNITINLSVSSQHGELVPVLAHEWTLQTDASILYLEGALSVLQLN 120
QY 121 TNERLCYKFOFLSMLOHRRKMRFSFSHFVVDPGQEVETVYHHLKRPDPGPNHRSKII 180
DB 121 TNERLCYKFOFLSMLOHRRKMRFSFSHFVVDPGQEVETVYHHLKRPDPGPNHRSKII 180
QY 181 FVPDCEDSKMKMTTSCVSSGSLMDPNITVETLDQHLRVDFLTLMNESTPYQVLLSEFSDS 240
DB 181 FVPDCEDSKMKMTTSCVSSGSLMDPNITVETLDQHLRVDFLTLMNESTPYQVLLSEFSDS 240
QY 241 ENHSCFVYVQIAPRQEEFORANVTFTLSKFHWCCHHHVQVOFFSSCLNDCLRHAAT 300
DB 241 ENHSCFVYVQIAPRQEEFORANVTFTLSKFHWCCHHHVQVOFFSSCLNDCLRHAAT 300
QY 301 VPCPVISNTTVPKPVADYIPLM 322
DB 301 VPCPVISNTTVPKPVADYIPLM 322

RESULT 8
US-09-022-257-2
Sequence 2, Application US/09022257
Patent No. 6197525
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation

STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022.257
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-257-2

Query Match 100.0%; Score 1766; DB 4; Length 864;
Best Local Similarity 100.0%; Pred. No. 1,1e-183;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIRRCPRVVPGALGMLLLNLVLAAGRASPRLDPAPVCAOEGISCRVKNSTCLDD 60
DB 1 MAIRRCPRVVPGALGMLLLNLVLAAGRASPRLDPAPVCAOEGISCRVKNSTCLDD 60
QY 61 SWIHPKMLTPSSPNITINLSVSSQHGELVPVLAHEWTLQTDASILYLEGALSVLQLN 120
DB 61 SWIHPKMLTPSSPNITINLSVSSQHGELVPVLAHEWTLQTDASILYLEGALSVLQLN 120
QY 121 TNERLCYKFOFLSMLOHRRKMRFSFSHFVVDPGQEVETVYHHLKRPDPGPNHRSKII 180
DB 121 TNERLCYKFOFLSMLOHRRKMRFSFSHFVVDPGQEVETVYHHLKRPDPGPNHRSKII 180
QY 181 FVPDCEDSKMKMTTSCVSSGSLMDPNITVETLDQHLRVDFLTLMNESTPYQVLLSEFSDS 240
DB 181 FVPDCEDSKMKMTTSCVSSGSLMDPNITVETLDQHLRVDFLTLMNESTPYQVLLSEFSDS 240
QY 241 ENHSCFVYVQIAPRQEEFORANVTFTLSKFHWCCHHHVQVOFFSSCLNDCLRHAAT 300
DB 241 ENHSCFVYVQIAPRQEEFORANVTFTLSKFHWCCHHHVQVOFFSSCLNDCLRHAAT 300
QY 301 VPCPVISNTTVPKPVADYIPLM 322
DB 301 VPCPVISNTTVPKPVADYIPLM 322

RESULT 9
US-08-620-694A-10
Sequence 10, Application US/08620694A
Patent No. 586286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286e1 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)387-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-620-694A-10

Query Match 71.0%; Score 1254; DB 2; Length 866;
Best Local Similarity 71.4%; Pred. No. 7.3e-128;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

1 MAIRRCMPRVYGPALGWLILLNLVLAAPGRASPRILDFPAPVCAQEGLSRVKNSCTCDD 60
1 MGAARSPSAVPRPLGLILLGLVLAAPGASLRLDLHRAVCSQPLNCVKNSTCDD 60
61 SWIHPKRLTPSSSKNIIYINLSVSTOGELVPVLAHEMTLOTDSILYLEGAELSVQLN 120
61 SWIHPKRLTPSSSKNIIYINLSVSTOGELVPVLAHEMTLOTDSILYLEGAELSVQLN 120
121 TNERLCVVKFOFLSMLOHHRKRWRFSEHFVVDPOGEYEVTVNHLPKPIPDGDPNHSKTI 180
121 TNERLCVVKFOFLSMLOHHRKRWRFSEHFVVDPOGEYEVTVNHLPKPIPDGDPNHSKTI 180
181 FVPDCEDSKMKMTTSCVSSGLMDPNITVETLDTQHLRVDFTLNNESTPYQVLLSESDS 240
181 FVPDCEDSKMKMTTSCVSSGLMDPNITVETLDTQHLRVDFTLNNESTPYQVLLSESDS 240
241 ENHSCFDDVYKQIAPROEEHORANVTFTLSKFWCCCHNHVOVOPFSSCLINDCLRHAVT 300
241 ENHSCFDDVYKQIAPROEEHORANVTFTLSKFWCCCHNHVOVOPFSSCLINDCLRHAVT 300
301 VPCPVNTVTPKPVADYIPLM 322
301 VPCPVNTVTPKPVADYIPLM 322
301 VSCPEMDT--PEIPIDYMPLM 320
301 VSCPEMDT--PEIPIDYMPLM 320

RESULT 10
US-09-022-255-10
Sequence 10, Application US/09022255
Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033e1 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-10

Query Match 71.0%; Score 1254; DB 3; Length 866;
Best Local Similarity 71.4%; Pred. No. 7.3e-128;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

1 MAIRRCMPRVYGPALGWLILLNLVLAAPGRASPRILDFPAPVCAQEGLSRVKNSCTCDD 60
1 MGAARSPSAVPRPLGLILLGLVLAAPGASLRLDLHRAVCSQPLNCVKNSTCDD 60
61 SWIHPKRLTPSSSKNIIYINLSVSTOGELVPVLAHEMTLOTDSILYLEGAELSVQLN 120
61 SWIHPKRLTPSSSKNIIYINLSVSTOGELVPVLAHEMTLOTDSILYLEGAELSVQLN 120
121 TNERLCVVKFOFLSMLOHHRKRWRFSEHFVVDPOGEYEVTVNHLPKPIPDGDPNHSKTI 180
121 TNERLCVVKFOFLSMLOHHRKRWRFSEHFVVDPOGEYEVTVNHLPKPIPDGDPNHSKTI 180
181 FVPDCEDSKMKMTTSCVSSGLMDPNITVETLDTQHLRVDFTLNNESTPYQVLLSESDS 240
181 FVPDCEDSKMKMTTSCVSSGLMDPNITVETLDTQHLRVDFTLNNESTPYQVLLSESDS 240
241 ENHSCFDDVYKQIAPROEEHORANVTFTLSKFWCCCHNHVOVOPFSSCLINDCLRHAVT 300
241 ENHSCFDDVYKQIAPROEEHORANVTFTLSKFWCCCHNHVOVOPFSSCLINDCLRHAVT 300
241 ENHSCFDDVYKQIAPROEEHORANVTFTLSKFWCCCHNHVOVOPFSSCLINDCLRHAVT 300

Db 181 LVPDEHARMKVTTPCMSSGSLMDPNITVETTLRAHOLRSFTLMNESTHQIILTSFPHM 240
QY 241 ENHSCFDVVKQIFAPROEEFHORANYFTLSKPFHWCCHHHVVOVOPFSSCLNDCRLRAVT 300
Db 241 ENHSCFEHHHHIIPARPEEFHORNSVTLRLNKGCCRHQVOIQOPFSSCLNDCRLRSAT 300
QY 301 VPCPVISNTTVKPVADYIPLM 322
Db 301 VSCPEMPDT--PEPIDYMLWM 320

RESULT 13

US-09-022-253-10
; Sequence 10, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-253-10

Query Match 71.0%; Score 1254; DB 3; Length 866;
Best Local Similarity 71.4%; Pred. No. 7.3e-128;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

QY 1 MATRCMPRVYVPGPALGMLLLNLVLAAGRASPRLDPPAPVCAOEGLSCRYKNSTCLDD 60
Db 1 MGAARSPSVAVPGGLLLLLGLVLAAPGASLRLLDHRALVCSQPGNLCTVKNSTCLDD 60
QY 61 SWIHPRLNLPSSPKNIYINLSVSTOGELVPLVHVEWTLQTDASILYLEGAELSVLQIN 120

Db 61 SWIHPRLNLPSSPKNDQIQDLHFVANHETLQTDASILYLEGAELSVLQIN 120
QY 121 TNERLCVAFQFSLMOHRRKRRFSFHYVDPGQEVYVHLPKPIPGDPRHKSII 180
Db 121 TNERLCVAFREFSLKLRHRRRMRFTHFVDPDQEVYVHLPKPIPGDPRHKSNF 180
QY 181 FVPCDEDSKMKMTSCVSSGSLMDPNITVETTLDTLHRAVDFTLMNESTPYOVILESPDS 240
Db 181 LVPDCHEARMKVTTPCMSSGSLMDPNITVETTLRAHOLRSFTLMNESTHQIILTSFPHM 240
QY 241 ENHSCFDVVKQIFAPROEEFHORANYFTLSKPFHWCCHHHVVOVOPFSSCLNDCRLRAVT 300
Db 241 ENHSCFEHHHHIIPARPEEFHORNSVTLRLNKGCCRHQVOIQOPFSSCLNDCRLRSAT 300
QY 301 VPCPVISNTTVKPVADYIPLM 322
Db 301 VSCPEMPDT--PEPIDYMLWM 320

RESULT 14

US-09-022-260-10
; Sequence 10, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-260-10

Query Match 71.0%; Score 1254; DB 3; Length 866;
Best Local Similarity 71.4%; Pred. No. 7.3e-128;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

QY	1	MAIRRCPRVAVGALMILNLTAVLAPGASPRILDEPRVCAOELSTCRVKNSTCLD	60
Db	1	MGAARSPSAVPGVLGVLILLGLLGLVLRPGASLRILDLHRLVYQSLQELNLTAVNSTCLDD	60
QY	61	SWIAPKULTPSSPKNIYINLVSSSTQNGELVLPVJHWEMLTQTDASILYLEGALSVQLN	120
Db	61	SWIHRNULTPSSRPDLDIQLFHATQGGDLFRVANIEMTLQTDASILYLEGALSVQLN	120
QY	121	TNERLCYKQFLSMLOHRRKRWRESFSHFVYVDRQGEYEVTVHHLKPIRPGDGNHKSII	180
Db	121	TNERLCYKQFLSKLRHHRRRWRTFSHFVYVDRQGEYEVTVHHLKPIRPGDGNHQSKN	180
QY	181	FVPRCEESKAKMTSCYSSGSLMDPNITVETLQHLKVDFTLMNESTPRVQVLLSEFSDS	240
Db	181	LVPCEEHARKVYVTPCMSGSLMDPNITVETLELBAHQLRVSEFTLMNESTHYQILLSTPHM	240
QY	241	ENHSCFPVUQIAPRQEEFHORANVFTLSKRWCCSHHNVQVOPRFSGLNDCILNAVT	300
Db	241	ENHSCFEMHNIIPRPREEFHQRNSVTLTLNRILKGCRCRHOVQIQPFFSSCLNDCILRSAT	300
QY	301	VPCVISTNTVVKPVADYIDLM 322	
Db	301	VSCPEMPDT---PEPIPYEMELM 320	

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 17, 2001, 11:17:26 ; Search time 26.59 seconds
(without alignments)
922.460 Million cell updates/sec

Title: US-09-488-728-2_COPY_1_322
Perfect score: 1766
Sequence: 1 MAIRRCMPRVPCGALGWL.....CPVISNTTPKPVADYIPLW 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	6.4	2311	1	kinase-related pro
2	112.5	6.4	708	2	probable transcrip
3	101	5.7	880	1	protein-tyrosine k
4	99.5	5.6	1506	2	Integumentary muc
5	99	5.6	449	2	gamma-aminobutyric
6	99	5.6	449	2	GABA receptor del
7	98	5.5	1748	2	probable membrane
8	97	5.5	880	2	protein-tyrosine k
9	95	5.4	449	2	gamma-aminobutyric
10	94	5.3	388	2	granulocyte/macrop
11	92	5.2	682	2	hypothetical prote
12	91.5	5.2	3131	2	vacuolar protein s
13	91	5.2	333	2	hypothetical prote
14	89.5	5.1	606	2	PF20 protein, micr
15	89.5	5.1	885	2	T16612.1 protein -
16	88.5	5.0	308	2	Ig heavy chain C r
17	88.5	5.0	472	2	Ig gamma-1 chain -
18	88.5	5.0	954	2	glucan 1,4-alpha-g
19	88	5.0	1231	2	protein-tyrosine-p
20	88	5.0	1323	2	coronin-like prote
21	87.5	5.0	416	2	hypothetical prote
22	87.5	5.0	577	2	Ig heavy chain - n
23	87.5	5.0	1188	2	pol polyprotein -
24	87	4.9	520	2	leukotriene-B4 20-
25	87	4.9	2515	2	interleukin-B4 20-
26	86.5	4.9	377	2	interleukin-1 beta
27	85.5	4.8	1164	2	DNA polymerase III
28	85	4.8	567	2	mcf2 protein - hum
29	85	4.8	925	1	transforming prote

30	84.5	4.8	429	1	EHRT	Ig epsilon chain C
31	84.5	4.8	712	2	T02312	hypothetical prote
32	84.5	4.8	1747	2	A45974	collagen alpha 1(X
33	84	4.8	243	2	S25755	Ig lambda chain -
34	83.5	4.7	304	2	B83541	probable polynucle
35	83.5	4.7	1213	2	A54063	TARA-binding prote
36	83	4.7	432	1	A41056	brachyury homolog
37	83	4.7	672	1	KIHUCA	protein kinase C (
38	83	4.7	672	1	KIRTC	protein kinase C (
39	83	4.7	672	1	KIMSCA	protein kinase C (
40	83	4.7	672	1	KIRBC	protein kinase C (
41	83	4.7	1038	2	S06046	integrin alpha-4 c
42	83	4.7	4688	2	F82885	hypothetical prote
43	82.5	4.7	318	2	S52424	homodomain protei
44	82.5	4.7	329	2	S00847	Ig gamma-2c chain
45	82.5	4.7	399	2	T41786	P47orf40 - Bombyx

ALIGNMENTS

RESULT 1
TVCNHR
kinase-related protein ros precursor - chicken
N:Alternate names: sevenless homolog c-ros
N:Contains: protein-tyrosine kinase (EC 2.7.1.112) ros
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1989 #sequence_revision 07-Oct-1994 #text_change 16-Jun-2000
C:Accession: A60197; A28357; A25225
R:Chen, J.; Heller, D.; Poon, B.; Kang, L.; Wang, L.H.
Oncogene 6, 257-264, 1991
A:Title: The proto-oncogene c-ros codes for a transmembrane tyrosine protein kinase s
A:Reference number: A60197; MUID:91156299
A:Accession: A60197
A:Molecule type: mRNA
A:Residues: 1-2311 <CHE>
A:Note: authors translated the codon GGA for residue 961 as Ser, AAT for residue 962
R:Podell, S.B.; Sefton, B.M.
Oncogene 2, 9-14, 1987
A:Title: Chicken proto-oncogene c-ros cDNA clones: identification of a c-ros RNA tran
A:Reference number: A28357; MUID:86143715
A:Accession: A28357
A:Molecule type: mRNA
A:Residues: 2010-2139, 'LP', '2142-2311' <POD>
A:Cross-references: GB:X06770; NID:963775; PIDN:CAA29938.1; PID:g1334743
R:Neckameyer, W.S.; Shibuya, M.; Hsu, M.T.; Wang, L.H.
Mol. Cell. Biol. 6, 1478-1486, 1986
A:Title: Proto-oncogene c-ros codes for a molecule with structural features common to
A:Reference number: A25225; MUID:87064428
A:Accession: A25225
A:Molecule type: DNA
A:Residues: 1868-2139, 'LP', '2142-2254', 'SSTKILRVSLGSAVPTAFAPQCNVNSONGMGKGP' <NEC>
A:Cross-references: GB:M13013; NID:9212636; PIDN:AAA49058.1; PID:g212637
C:Genetics:
A:Gene: ros
C:Superfamily: kinase-related protein ros; LDL receptor WYTD-containing repeat homolo
C:Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferas
E:1-27/Domain: signal sequence #status predicted <SIG>
E:28-2311/Product: kinase-related protein ros #status predicted <AT>
F:28-1873/Domain: extracellular #status predicted <EXT>
F:344-387/Domain: LDL receptor WYTD-containing repeat homology <YW1>
F:475-512/Domain: LDL receptor WYTD-containing repeat homology <YWA>
F:715-758/Domain: LDL receptor WYTD-containing repeat homology <YWB>
F:759-799/Domain: LDL receptor WYTD-containing repeat homology <YWC>
F:800-839/Domain: LDL receptor WYTD-containing repeat homology <YWD>
F:844-889/Domain: LDL receptor WYTD-containing repeat homology <YWE>
F:894-934/Domain: LDL receptor WYTD-containing repeat homology <YWF>
F:1546-1587/Domain: LDL receptor WYTD-containing repeat homology <YWG>
F:1874-1899/Domain: transmembrane #status predicted <TMN>
F:1800-2311/Domain: intracellular #status predicted <INT>
F:1859-2233/Domain: protein kinase homology <KIN>
F:1967-1975/Region: protein kinase ATP-binding motif
F:49,65,77,123,132,265,287,307,333,377,480,607,628,706,714,911,940,962,971,1110,1154,

ent) #status predicted
F:1996/Active site: Lys #status predicted
F:2127/2131,2132/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #stat

[illegible]

```

RESULT      2
T50064
Probable transcription activator [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: T50064
R:Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, February 2000
A:Reference number: Z25032
A:Accession: T50064
A:Status: preliminary; translated from GB/EMBL/DBDy
A:Molecule type: DNA
A:Residues: 1708 <HAR>
A:Cross-references: EMBL:AL157994; PIDN:CAR76236.1; GSPDB:GN00066; SPDB:SPAC105.03c
A:Experimental source: strain 972h(-); cosmid c105
C:Genetics:
A:Gene: SPDB:SPAC105.03c
A:Map position: 1

```

```

Query Match      6.48; Score 112.5; DB 2; Length 708;
Best Local Similarity 21.6%; Pred. No. 0.19;
Matches 63; Conservative 45; Mismatches 78; Indels 105; Gaps

QY 44 ADEGLSCRVNKTCL-----DDSWIHPKMLTPSSPKNIYTNL-----SY 82
    ||| |||
Db 14 AGPNLCIPCSIGTCLIFHEHRESSFMDFVSLFCSSP--YENLPPhRSSSLSEKKPSV 70
    ||| |||
QY 83 SS-----TOGELAVPLVHVE---WLIQDASILLEGAGLSVLQLTNTNERLCV 127
    :||| :||| :||| :||| :||| :|||
Db 71 ASODVKSDELPICTNNNPFLPHSQQESHWTIRHESMPALSALGSSAQSMQ----- 121
    :||| :||| :||| :||| :||| :|||
QY 128 KFOFLSMLOHHRK-RWRFSFHFVVDPQOEYEVTVAHLHKPT-----EDGENHRSKIT 180
    ||| :||| :||| :||| :||| :|||
Db 122 -GEPSITQNEENFRFKSFQ-----POPIVKETTFPKSEBGGQEHAKL 163
    :||| :||| :||| :||| :||| :|||
QY 181 -----FVPCEDSKMKMTI-----SCVSGSLMDPVIVT-----ETIDTOLRNVDTL 223
    :||| :||| :||| :||| :||| :|||
Db 164 SDSLSEYERLKYSSTKKEVRSEADPPSPSLNSTVDLDNDSDLSIQGSSVDDC--TDFFLG 220

```

```

QY      224 WNESTPYQVLLLESFSDSENHSCFEDVAKQIFAPROEEFHQRANVTFTLSKFH 274
      ::: | :| |:: |::: | |:: |::| |
Db      221 FDSLSYAYILNPSTDSD---VDLIRQYFIPEKG-----TYTFSNMH 259

```

RESULT 3

JC4166
N:Alternate names: protein-tyrosine kinase (EC 2.7.1.112) tyro3 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JC4166; PTO185
J.T. Biochem. 117, 1267-1275, 1995
A>Title: Molecular cloning and in situ localization in the brain of rat Sky receptor
A:Reference number: JC4166; MVID:96104999
A:Accession: JC4166
A:Molecule type: mRNA
A:Residues: 1-880 <OH>
A:Cross-references: DDBJ:D37880; NID:g1498195; PIDN:BAO7119.1; PID:g829057
A:Experimental source: brain
A>Note: It is uncertain whether Met-1 or Met-7 is the initiator
R:Lai, C.; Lemke, G.
Neuron 6, 691-704, 1991
A>Title: An extended family of protein-tyrosine kinase genes differentially expressed
A:Reference number: PTO183; MVID:91222560
A:Accession: PTO185
A:Molecule type: mRNA
A:Residues: 650-703 <LA1>
A:Experimental source: sciatic nerve
C:Comment: This receptor plays an important role in development, function, and maintenance:
C:Genetics:
S:Gene: tyro-3
C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; immunoglobulin domain
K:Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transformant
F:1-31/Domain: (or 7-31) signal sequence #status predicted <SIG>
F:52-880/Product: (or 32-874) protein-tyrosine kinase tyro3 #status predicted <MAT>
F:50-109/Domain: immunoglobulin homology <IMM1>
F:146-195/Domain: immunoglobulin homology <IMM2>
F:214-299/Domain: fibronectin type III repeat homology <FN3>
F:312-395/Domain: fibronectin type III repeat homology <FN3B>
F:419-441/Domain: transmembrane #status predicted <TM>
F:506-783/Domain: protein kinase homology <Kin>
E:514-522/Region: protein kinase ATP-binding motif
F:515-766/Domain: cytoplasmic tyrosine kinase #status predicted <CTX>
E:533-755/Binding site: carbohydrate (Asn) (covalent) #status predicted <CTK>

```

Query Match Similarity      5.7%; Score 101; DB 1; Length 880;
Best Local Similarity      21.4%; Pred No. 2,2; Mismatches 129; Indels 104; Gaps 19;
Matches      78; Conservative      53;

```


Db 55 SVEGMEDPDIMMKGITVYQNAHQ-----VSIISIEH-SWIGLILSKVERSDAGLWQC 108
QY 111 GAELSVTLQNTNERLCVKEQFLSMLOHHRKRWRFSESHVVPD----- 153
Db 109 VKDGEETKISQSVMLTVE-----GVPEFTVEKDLAVPNAFQLSCEA 152
QY 154 -GQEVETVNHLPKPIPGDDPNHKKIIFVP-----DCEDSKMK-WTTSVSSGSLM 203
Db 153 VGPEPEPVITVYWRGLTKVGGAPSPSVLNVGVTQRTESFCARNTKGLATSRPAIVRLQ 212
QY 204 DP-----NITVETLDTQHLRVDFLTLMNESTPYQVLLESFSDENHSCFVVKQIFAPROE 258
Db 213 APPAPPEFTVTTTSSVNASV---AWPFGADGLALL-----HSC--TVQYAHAP--G 257
QY 259 EFHORANVTFTLSKFWCHHVVQVQPEFSSC-----LNDCLRHAAYVPCPVISNTVTPKP 314
Db 258 EWEALAVV-----VVPFPP--TCLLNKLAPATVYSLRVRC---ANALGPSP 258
QY 315 VADYIP 320
Db 299 YGDWVP 304

RESULT 9
A34625
gamma-aminobutyric acid/benzodiazepine receptor type A delta chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 20-Aug-1999
C:Accession: A34625; A58811; J00076
R:Zhao, Z.; Jono, R.H.
Biochem. Biophys. Res. Commun. 167, 174-182, 1990
A:Title: Isolation of distantly related members in a multigene family using the polymerase chain reaction
A:Reference number: A34625; MUID:90179746
A:Accession: A34625
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-449 <ZNA>
A:Cross-references: GB:M5162; NID:g204207; PID:AAA1182.1; PID:g204208
R:Motiejlek, K.; Haenselmann, R.; Leitgeb, S.; Luescher, B.
J. Biol. Chem. 269, 15265-15273, 1994
A:Title: BSL1, a novel brain-specific DNA-binding protein recognizing a tandemly repeated sequence
A:Reference number: A53811; MUID:94255091
A:Accession: A53811
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-26 <MOT>
A:Cross-references: GB:X69986
R:Shivers, B.D.; Killisch, I.; Sprengel, R.; Sontheimer, H.; Koehler, M.; Schofield, P.R.
Neuron 3, 327-337, 1989
A:Title: Two novel GABA-A receptor subunits exist in distinct neuronal subpopulations.
A:Reference number: J00076; MUID:90380375
A:Accession: J00076
A:Molecule type: mRNA
A:Residues: 1-92, 'RA', 95-130, 'VCLV', 135-403, 'VP', 406-449 <SHI>
A:Experimental source: brain
C:Comment: Neurotransmission effected by gamma-aminobutyric acid (GABA) is mediated mainly by GABA-A receptors. The GABA-A receptor consists of subunits that are structurally related to 11g C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-449/Product: gamma-aminobutyric acid A receptor delta chain #status predicted <MAT>
F:249-271/Domain: transmembrane #status predicted <TM1>
F:275-297/Domain: transmembrane #status predicted <TM2>
F:309-331/Domain: transmembrane #status predicted <TM3>
F:427-449/Domain: transmembrane #status predicted <TM4>
F:103,106/Binding site: carboxylate (Asn) (covalent) #status predicted
F:164-178/Disulfide bonds: #status predicted

Query Match 5.4%; Score 95; DB 2; Length 449;
Best Local Similarity 22.2%; Pred. No. 3;
Matches 63; Conservative 44; Mismatches 85; Indels 92; Gaps 17;

QY 16 LGWLLLLNLVLPGRASRLDPPAPVCAQEGLSRVKN-----STCLDSWI----- 63
Db 4 LGWLL-----PLTL-----LCTPHHGARAMNDIGDYGSNLEISMLPNDGL 47
QY 64 ---HPKNTLP---SSPKIYINLSVSSPHQHGELVVLVHEVTLQTDASLTLEGALSL 117
Db 48 MEGYARNRFRGIGPPVNVVALALEVASTDH---ISEANNEYMTV---FLHOSWRGRSL 101
QY 118 QLTNTERLCVKEQFLSMLOHHRKRWRFSESHVVPDQGE--YEYTVNH-LPKPIPDGDN 174
Db 102 YNHTNETLIGDSRVYDKL-----WLPDFTYAKSAGMFHDYVENKILRLQPDG--- 150
QY 175 HKSKIIIFVPCDESKMKMTTSCVSSGSLMDPNITVETLDTQHLRVDFLTLMNESTPYQVLL 234
Db 151 ---VILY-----SIRITSTVAC-----DMDLAKVPMDEQCMID-----L 182
QY 235 ESEFSDENHSCFVDYKQIFARQEEFH-----QRANVTFTLSKF 273
Db 183 ESY-----GYSESDIV-YVWSENQEOIHGIDRLQLAQFTITSYRF 221

RESULT 10
A45304
granulocyte/macrophage colony-stimulating factor receptor, low affinity, precursor - :
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C:Accession: A45304
R:Park, L.S.; Martin, U.; Sorensen, R.; Lühr, S.; Morrissey, P.J.; Cosman, D.; Larsen
Proc. Natl. Acad. Sci. U.S.A. 89, 4299-4299, 1992
A:Title: Cloning of the low-affinity murine granulocyte-macrophage colony-stimulating factor receptor
A:Reference number: A45304; MUID:92262426
A:Accession: A45304
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-388 <PAR>
A:Cross-references: GB:M85078; NID:g192594; PID:AAA37421.1; PID:g192595
C:Keywords: transmembrane protein

Query Match 5.3%; Score 94; DB 2; Length 388;
Best Local Similarity 21.6%; Pred. No. 3;
Matches 68; Conservative 35; Mismatches 108; Indels 104; Gaps 15;

QY 5 RCWPR-----VVPFGALGWLILLNLVLPGRASRLDPPAPVCAQEGLS 49
Db 88 RCWPRRMALHGVTLVDYNGVGGAAHWRSLFVESAAGSA-----ENLT 134
QY 50 CRYKNSITCLDDSWTHPKNLTPSSPKNIYINLSV-SSIQH-----GELVPLVHEWT 99
Db 135 CEIRAAFLSCAW---REGPAAPADVRYSLRLNLSGHDVARCMADPCDDV----ITQC 186
QY 100 LQTDASLTLEGALSVQLTNERLCVKE-----QFLSM-----QHKK 140
Db 187 IANDLSL---GSEAYILVTVGRSGAGPVRLDDVATKALTEKLGPPRDVTASCNSHCTV 243
QY 141 RW-----RFSFHFVVDQGE-----YEYTVNHLPKPIPDGPPNHSKII 180
Db 244 SWAPPSTWASLTARDPQEVOMQSAPEGSTPRKVLVETRLAFSPAPNG--GKVKV- 300
QY 181 FVPDCESKMKMTTSCVSSGSLMDPNITVETLDTQHLRVDFLTLMNESTPYQVLLESFSDS 240
Db 301 ---RAGDTRMK-----HMGWESPANHLEAEDT---RVPGALIVAVACAVILCALALG 347
QY 241 ENHSCFVDYKQIFAP 255
Db 348 VTCRRFEVTRRLFP 362

RESULT 11
G86300
hypothetical protein A610824.1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

DB 260 KLADHTIPDQED-----GEGALLENGV

RESULT 14
T08180
PF20 protein, microtubule-associated - Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: T08180
R:Smith, E.; Lefebvre, P.
submitted to the EMBL Data Library, November 1996
A:Description: The PF20 gene product contains WD repeats and localizes to the inter-mic
A:Reference number: Z16400
A:Accession: T08180
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-606 <SMI>
A:Cross-references: EMBL:U78547; NID:g1813637; PID:g1813638
C:Genetics:
A:Gene: PF20
A:Keywords: microtubule

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 17, 2001, 11:15:41 ; Search time 34.56 Seconds
(without alignments)
564,842 Million cell updates/sec

Title: US-09-488-728-2_COPY_1_322
1766
Sequence: 1 MAIRCMRPVVPGPALGML.....CPVISNTVPKPYADYIPLW 322

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

A_Geneseq_0601:*

- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT:*
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- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1766	100.0	330	21	AA97255 Soluble IL-17R/Fla
2	1766	100.0	330	21	AA97258 Soluble IL-17R/Fla
3	1766	100.0	864	17	AAW04184 Murine Interleukin-
4	1766	100.0	864	19	AAW61271 Mouse Interleukin-
5	1766	100.0	864	20	AAW92408 Murine IL-17R prot
6	1766	100.0	864	21	AAW99335 Murine IL-17R prot
7	1766	100.0	864	21	AAW97130 Murine Interleukin
8	1766	100.0	864	21	AAW97180 Murine Interleukin
9	1766	100.0	864	21	AAW03806 Murine Interleukin
10	1766	100.0	864	22	AAW62060 Murine IL-17R poly
11	1766	100.0	864	22	AAW72748 Murine Interleukin

12	1254	71.0	866	17	AAW04185	Human Interleukin-
13	1254	71.0	866	19	AAW61272	Human Interleukin-
14	1254	71.0	866	20	AAW92409	Human IL-17R prote
15	1254	71.0	866	21	AAW99941	Human IL-17R prote
16	1254	71.0	866	21	AAW97131	Human Interleukin-
17	1254	71.0	866	21	AAW97181	Human Interleukin-
18	1254	71.0	866	21	AAW97180	Human Interleukin-
19	1254	71.0	866	22	AAW62060	Human IL-17R (hCTL
20	1254	71.0	866	22	AAW72754	Human Interleukin-
21	1254	71.0	426	21	AAW18750	A human Interleuki
22	282.5	16.0	426	21	AAW70591	Interleukin 17-lik
23	282.5	16.0	426	21	AAW49946	Human Interleukin
24	282.5	16.0	433	21	AAW18754	A human Interleuki
25	282.5	16.0	433	21	AAW70595	Interleukin 17-lik
26	282.5	16.0	502	22	AAW87604	Human PRO5801. Ho
27	208.5	11.8	385	21	AAW825795	Human secreted pro
28	208.5	11.8	385	22	AAW75381	Human secreted pro
29	137	7.8	34	20	AAW39426	Human Interleukin-
30	97	5.5	880	16	AAW77846	Mouse Rse rPTK. M
31	95.5	5.4	977	22	AAW31164	Amino acid sequenc
32	92	5.2	729	21	AAW44857	Mouse taste cell s
33	88	5.0	874	15	AAW60545	Murine development
34	88	5.0	874	19	AAW79145	Receptor protein t
35	88	5.0	874	20	AAW81402	Receptor protein t
36	88	5.0	993.	6	AAW50116	Sequence of Hepati
37	86.5	4.9	377	16	AAW84740	Interleukin-1-beta
38	86.5	4.9	377	17	AAW88750	Human Tx protease,
39	86.5	4.9	377	17	AAW00213	Human Ich-2 protei
40	86.5	4.9	377	17	AAW80702	Interleukin-1-beta
41	86.5	4.9	377	20	AAW21718	Human IL-17R
42	86	4.9	322	20	AAW14072	Amino acid sequenc
43	84.5	4.8	340	21	AAW03643	Human BS247 specif
44	84.5	4.8	565	16	AAW6700	Rat IgE heavy chai
45	84	4.8	452	17	AAW97299	E1ET enterotoxin e

ALIGNMENTS

RESULT 1	AA97255	standard; peptide: 330 AA.
ID	AA97255	
XX	AA97255;	
AC	AA97255;	
XX		
DT	04-DEC-2000	(first entry)
XX		
DE	Soluble IL-17R/Flag fusion protein.	
XX		
KW	IL-17R; Interleukin-17 receptor; soluble; CTLA-8; Herpesvirus salmriti;	
KM	HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;	
KW	anti-asthmatic; flag epitope; fusion protein.	
XX		
OS	Mus sp.	
XX		
FT	Key	Location/Qualifiers
FT	Protein	1..322
FT		/label= Soluble_IL-17_receptor
FT	Peptide	1..31
FT		/label= Signal_peptide
FT	Protein	32..322
FT		/label= IL-17_receptor_extracellular_domain
FT	Peptide	323..330
FT		/label= Flag-epitope
XX		
PN	US6096305-A.	
XX		
PD	01-AUG-2000.	
XX		
PF	11-FEB-1998;	98US-0022253.
XX		
PR	21-MAR-1996;	96US-0620694.
PR	23-MAR-1995;	95US-0410535.

```

XX 07-AUG-1995;      95US-0538765.
XX FA              (IMMV ) IMMUNEX CORP.
XX PI              Fanslow WC, Springs MK, Yao Z;
XX DR              WPI: 2000-523862/47.
XX
PT Suppressing rejection of a grafted syngeneic or allogeneic organ or
PT tissue in a graft recipient for organ transplantation involves
PT transecting the organ or tissue with DNA encoding soluble
PT interleukin-17R receptor
XX
PS Example 3; Column -: 27bp; English.
XX
CC A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC cDNA library from T cell thymoma EL4 cells, which were identified as
CC binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC region and soluble IL-17 (CTLA-8) protein or a homologous
CC Herpesvirus saimiri (HSV) protein, designated HSV13. Suppressing
CC rejection of a grafted syngeneic or allogeneic organ or tissue in a
CC graft recipient involves transfecting the organ or tissue to be
CC transplanted with DNA encoding soluble IL-17R, so that expression of
CC IL-17R by the engrafted organ or tissue results in suppression of
CC rejection. Soluble IL-17R fragments comprise residues 1-322 of the murine
CC IL-17R, residues 1-320 of the human IL-17R, and fragments of the
CC extracellular domain that bind IL-17. The method is useful for regulating
CC an immune response, for suppressing rejection of grafted organs or tissues
CC in the recipient and for treating or preventing diseases like allergy,
CC asthma and autoimmune diseases.
CC Note: This sequence does not appear in the specification. It was created
CC from the full length murine IL-17R (see AA97180) and the flag peptide
CC (see AA97183)
XX
SQ Sequence      330 AA;
XX
Query Match          100.0%; Score 1766; DB 21; Length 330;
Best Local Similarity 100.0%; Pred. No. 2,2e-169;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   1 MAIRRCWRVVVPGPALGWLLILLNLVLARGRASPRLLDPAPVCAOEGLSCKRNKSTCIDD 60
D   1 mairrcwrvvpgpalgwllillnlvlargrasprlldfapvcadeglsckrnkstcid 60
QY   61 SWIHPKNLTSPSPKKITVINL SVSFTQHGEELVYLHVEWTLIQDASITLYDEGAELSYQLN 120
D   61 swihpknltpsspkriylnlsvsftqhgeelvylylhvewtliqdasitlydegelsylqln 120
QY   61 swihpknltpsspkriylnlsvsftqbhelvpylvlnvetrlgtdaaillylegelsylvqln 120
QY  121 TNERLCVKFQFLSLMLQHHRRKRWFSEFSHFVVDVGGEYEVTYVHHLKRP1PDGDPNHKSKII 180
D  121 tnerlcvkfgflslmlqhhrrkrwfsefsfhfvvdvggeyevtvhhlkripdpdgdpnhkskii 180
QY  121 tnerlcvkfgflslmqhnkrkwrfsfshfvvdvggeyevtvhhlkripdpdgdpnhskii 180
QY  181 FVPPOCEDSRMKMTQTSVCVSSGSIMDNINIVETLDIQLRKDFLIWMNESTRYQVLLSFSDS 240
D  181 fvpdcedsrkmmttsvcvssgsimdnivetldtqlrkdflwmnestryqvllsfds 240
QY  181 fvpdcedskmmttsvcvssgsimdnivetldtqnltvdfilwmesrtyqvllsfds 240
QY  241 ENHSCEFDVVKQIFAPROEEFHORANVETLTLSKFHMCHCHHVGVOPFFSCINDCKLRHAVT 300
D  241 enhscfdvvkqifaproeefhoranvetltlskfhmchchhvovpffscindcklrhavt 300
QY  241 enhscfdvvkqifaprggefingranvttflskfnwcchhhgvavpfisscindclrhavt 300
D  241 vpcpviasntvvrkvadvyrplw 322
QY  301 VPCPVIASNTVVRKVADVYRPLW 322
D  301 vpcpviasntvvrkpadvyrplw 322
XX
RESULT      2
ID AA97258 standard; peptide: 330 AA.
XX
XX AA97258;
XX
DT 04-DEC-2000 (first entry)
```

Query Match	Best Local Similarity	Matches 322; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;
DB	1	MAIRRCWPRVVGPAALGMLLLILNVLAPGRASPRLLDPAPVCAEGISCRVKNSTCDD 60
QY	61	SWIHRKNLTSPSPKKIYIINTLSVSTOHELVPVLHVEWTLLQTDASILVLEGAELSVLQIN 120
DB	61	swihpknltspspkhiylnlsvstqhgelypvlhventldqdasillylegaelsvlqln 120
QY	121	TNERLCVAFQELSLQHHRRKMRSEFSHEVVDGQDEITYVHHLPKPIPDGDPNHKSII 180

```
Db 121 tnerlcvkfgflsmqlghrkrwrfsfshfvdpqgeyevtvhlpkpi pdgdpnhskii 180
OY 181 FVPDCEDSKMKMTTSCVSSGSLMDPNITVEITLDIQLRVDFLTWNESTPYQVLLSEFSDS 240
Db 181 fvpdcetskmkmttscvssgslwdpnlvteltdqhlrvdfllwnestryvllsefsds 240
OY 241 ENHSCFDPVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHWQVQPFSSCLNDCLRHAYT 300
Db 241 enhscfdvkvqifaprqeeffqranvftlskfhwcchhvwqvpffsscldncrlrhavt 300
OY 301 VPCPVISNTVTPKPVADYIPLM 322
Db 301 vpcpvlsntvtvpkpvadyiplw 322

RESULT 3
ID AAM04184 standard; Protein: 864 AA.
AC AAM04184;
XX
XX
XX 05-DEC-1996 (first entry)
DE Murine interleukin-17 receptor.
XX
XX Interleukin-17 receptor; IL-17R; autoimmune disease; allergy;
XX asthma; graft rejection; inflammation; cytokine; therapy.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX FH 1..31
XX FT /label= Sig-peptide
XX FT Domain 32..322
XX FT Domain /label= Extracellular_domain
XX FT Domain 323..343
XX FT Domain /label= Transmembrane_domain
XX FT Domain 344..864
XX FT /label= Cytoplasmic_tail
XX
XX W09629408-A1.
XX
XX 26-SEP-1996.
XX
XX 21-MAR-1996; 96MO-US04018.
XX
XX 07-AUG-1995; 95US-0538765.
XX 23-MAR-1995; 95US-0410535.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Fanslow WC, Spriggs MK, Yao Z;
XX
XX WPI; 1996-443184/44.
XX
XX N-PSDB; AAT33800.
XX
XX DNA encoding interleukin-17 receptor - useful for regulating immune
XX and inflammatory responses, or to suppress graft rejection
XX
XX Claim 1; Page 29-32; 52pp; English.
XX
XX The murine interleukin-17 receptor (IL-17R) (AAM04184) is a type I
XX transmembrane protein that binds IL-17 (CITA-8, see also AAM02386)
XX and HSV13 (AAM02387), a viral homologue of IL-17. Its amino acid
XX sequence was deduced from a cDNA clone (AAT33800) isolated from murine
XX thymoma EL4 cells. Soluble, recombinant forms of the receptor
XX (partic. amino acids 1-322) can be prep'd. in transformed host cells
XX and used to regulate immune and inflammatory responses, in methods
XX for suppressing rejection of grafted organs or tissue, and in
XX assays of IL-17 and IL-17R.
XX
XX Sequence 864 AA;
XX
XX
```

```
Query Match 100.0%; Score 1766; DB 17; Length 864;
Best Local Similarity 100.0%; Pred. No. 8,6e-169;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAIRRCWPRVVPALGMLLLNLVLAFCRASPRLLDPAPVCAOEGISCRVKNSTCIDD 60
Db 1 mairrcwprvvpagalgwllllnlvlapgrasprlldfpapcagegiscrvknstcid 60
OY 61 SWIHPKMLTSPSPKNITVNLVSSVQHGELVPLVHEVTIQDASTLYEGAEISYIQDN 120
Db 61 swihpkmltspspknitvnlvssvqhgelyplvhevltiqdasillyegaelisyiqdn 120
OY 121 TNERLCVKFQFLSMLOHRRKRMREFSFHFVVDPGQGEYEVTVHHLPKPIPDGDPNHKSKII 180
Db 121 tnerlcvkfgflsmqlghrkrwrfsfshfvdpqgeyevtvhlpkpi pdgdpnhskii 180
OY 181 FVPDCEDSKMKMTTSCVSSGSLMDPNITVEITLDIQLRVDFLTWNESTPYQVLLSEFSDS 240
Db 181 fvpdcetskmkmttscvssgslwdpnlvteltdqhlrvdfllwnestryvllsefsds 240
OY 241 ENHSCFDPVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHWQVQPFSSCLNDCLRHAYT 300
Db 241 enhscfdvkvqifaprqeeffqranvftlskfhwcchhvwqvpffsscldncrlrhavt 300
OY 301 VPCPVISNTVTPKPVADYIPLM 322
Db 301 vpcpvlsntvtvpkpvadyiplw 322
```

```
RESULT 4
ID AAM61271 standard; Protein: 864 AA.
AC AAM61271;
XX
XX 12-OCT-1998 (first entry)
DE Mouse interleukin-17 receptor.
XX
XX Interleukin-17 receptor; IL-17 receptor; mouse; nitric oxide;
XX cartilage; osteoarthritis; autoimmune disease; inflammation;
XX therapy.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX FH 1..31
XX FT /label= Sig-peptide
XX FT Protein 32..864
XX FT Protein /label= Mat_protein
XX FT Protein 1..322
XX FT /label= Soluble_IL-17R
XX FT /note= "Claim 2(a) "
XX FT Domain 32..322
XX FT Domain /label= Extracellular
XX FT Domain 323..343
XX FT Domain /label= Transmembrane
XX FT Domain 344..864
XX FT /label= Extracellular
XX
XX W09823284-A1.
XX
XX 04-JUN-1998.
XX
XX 21-NOV-1997; 97MO-US21451.
XX
XX 27-NOV-1996; 96US-0052525.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Trout AB;
XX
XX
```

XX WPI: 1998-322457/28.
 DR N-PSDB; AAV27591.
 XX Reducing nitric oxide production by cartilage associated cells - by
 PT contacting cells with soluble interleukin-17 receptor, useful to
 PT treat osteoarthritis and autoimmune and inflammatory diseases
 XX
 PS Claim 2(a): Page 20-23; 41pp; English.
 XX This polypeptide comprises mouse full-length interleukin-17
 CC receptor (IL-17R). A claimed method for reducing the amount of
 CC nitric oxide produced by a cartilage associated cell comprises
 CC contacting the cell with a soluble IL-17R, especially claimed
 CC soluble murine or human (see AAV61272) IL-17R comprising the signal
 CC peptide and extracellular domains of the respective full-length
 CC receptors. Recombinant soluble IL-17R polypeptides can be obtained
 CC using prokaryotic or eukaryotic (for glycosylated products)
 CC expression systems. A cDNA sequence (see AAV27591) coding for
 CC full-length murine IL-17R is provided. IL-17 is known to stimulate
 CC nitric oxide production from cartilage-associated cells in
 CC individuals with osteoarthritis. Inhibitors of nitric oxide
 CC production, such as soluble IL-17R, may therefore be useful to
 CC ameliorate the effects of nitric oxide in osteoarthritis as well
 CC as in other disease conditions in which nitric oxide plays a role,
 CC e.g. autoimmune and inflammatory diseases.
 XX
 SQ Sequence 864 AA:
 Query Match 100.0%; Score 1766; DB 19; Length 864;
 Best Local Similarity 100.0%; Pred. No. 8.6e-169;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAIRRCMPRVVPALGWLILNLVLAAPGRASPRILDFPAPVCAOEGISCRVKNSTCIDD 60
 DB 1 MAIRRCMPRVVPALGWLILNLVLAAPGRASPRILDFPAPVCAOEGISCRVKNSTCIDD 60
 QY 61 SMHPRKNIPLPSSPKNIIYNLSVSTQHGELVPVLAHVMTLOTDASTLYLEGAELSVQLN 120
 DB 61 SMHPRKNIPLPSSPKNIIYNLSVSTQHGELVPVLAHVMTLOTDASTLYLEGAELSVQLN 120
 QY 121 TNERLCVCKFOFLSMLOHRRKRMRFSESHFVDPQGEVTVNHLPKPIPDGDPNHSKII 180
 DB 121 TNERLCVCKFOFLSMLOHRRKRMRFSESHFVDPQGEVTVNHLPKPIPDGDPNHSKII 180
 QY 181 FVPDCEDSKMKTSCVSSGSLMDPNITVEITDQHLRVDFTMNESPXYOLLESFSDS 240
 DB 181 FVPDCEDSKMKTSCVSSGSLMDPNITVEITDQHLRVDFTMNESPXYOLLESFSDS 240
 QY 241 ENHSCFDVVKQIAPAPROEERHORANVTFTLSKFMCHHNVQVOPFSSCINDCLRHAVT 300
 DB 241 ENHSCFDVVKQIAPAPROEERHORANVTFTLSKFMCHHNVQVOPFSSCINDCLRHAVT 300
 QY 301 VPCPVISNTTVPKPVADYIPLW 322
 DB 301 VPCPVISNTTVPKPVADYIPLW 322
 RESULT 5
 AAW92408
 ID AAW92408 standard; Protein; 864 AA.
 AC AAW92408;
 DT 21-APR-1999 (first entry)
 DE Murine IL-17R protein.
 DE IL-17R: murine; interleukin-17 receptor; immunoregulator; inhibitor;
 KW T cell proliferation; T cell activation; organ; graft; rejection;
 KW autoimmune disease; allergy; asthma; treatment; inflammatory disease;
 KW B cell proliferation; immunoglobulin secretion; immunogen.

XX Mus sp.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..31
 FT /Label= signal_peptide
 FT Protein 32..864
 XX
 PN US5869286-A.
 XX
 PD 09-FEB-1999.
 XX
 PF 21-MAR-1996; 96US-0620694.
 XX
 PR 21-MAR-1996; 96US-0620694.
 PR 23-MAR-1995; 95US-0410535.
 PR 07-AUG-1995; 95US-0538765.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Fanslow WC, Spriggs MK, Yao Z;
 XX
 DR WPI: 1999-152766/13.
 DR N-PSDB; AAX01921.
 XX
 PT Isolated interleukin-17 receptor DNA - used to develop products for
 PT treating e.g. organ or graft rejection, autoimmune disease, allergy,
 PT asthma or inflammatory disease
 XX
 PS Disclosure; Column 25-30; 25pp; English.
 XX
 SQ This sequence represents a murine interleukin-17 receptor (IL-17R).
 CC IL-17R polypeptides have immunoregulatory activity. They can be used for
 CC inhibiting T cell proliferation, or for inhibiting T cell activation. In
 CC particular they can be used for preventing or treating organ or graft
 CC rejection, autoimmune disease, allergy or asthma. They can also be used
 CC for the prevention or treatment of inflammatory disease in which
 CC activated T cells play a role or for inhibiting B cell proliferation
 CC or immunoglobulin secretion. The IL-17 polypeptides can also be used
 CC as immunogens, reagents in in vitro assays, or as binding agents for
 CC affinity purification procedures.
 XX
 SQ Sequence 864 AA:
 Query Match 100.0%; Score 1766; DB 20; Length 864;
 Best Local Similarity 100.0%; Pred. No. 8.6e-169;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAIRRCMPRVVPALGWLILNLVLAAPGRASPRILDFPAPVCAOEGISCRVKNSTCIDD 60
 DB 1 MAIRRCMPRVVPALGWLILNLVLAAPGRASPRILDFPAPVCAOEGISCRVKNSTCIDD 60
 QY 61 SMHPRKNIPLPSSPKNIIYNLSVSTQHGELVPVLAHVMTLOTDASTLYLEGAELSVQLN 120
 DB 61 SMHPRKNIPLPSSPKNIIYNLSVSTQHGELVPVLAHVMTLOTDASTLYLEGAELSVQLN 120
 QY 121 TNERLCVCKFOFLSMLOHRRKRMRFSESHFVDPQGEVTVNHLPKPIPDGDPNHSKII 180
 DB 121 TNERLCVCKFOFLSMLOHRRKRMRFSESHFVDPQGEVTVNHLPKPIPDGDPNHSKII 180
 QY 181 FVPDCEDSKMKTSCVSSGSLMDPNITVEITDQHLRVDFTMNESPXYOLLESFSDS 240
 DB 181 FVPDCEDSKMKTSCVSSGSLMDPNITVEITDQHLRVDFTMNESPXYOLLESFSDS 240
 QY 241 ENHSCFDVVKQIAPAPROEERHORANVTFTLSKFMCHHNVQVOPFSSCINDCLRHAVT 300
 DB 241 ENHSCFDVVKQIAPAPROEERHORANVTFTLSKFMCHHNVQVOPFSSCINDCLRHAVT 300
 QY 301 VPCPVISNTTVPKPVADYIPLW 322
 DB 301 VPCPVISNTTVPKPVADYIPLW 322

RESULT 6
AA99935
ID AAY99935 standard; Protein; 864 AA.
XX
AC AAY99935;
XX
DF 10-JAN-2001 (first entry)
XX
DE Murine IL-17R protein.
XX
IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS 13;
KW murine; antibody; immune suppression.
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..31
FT Domain /label= Signal_peptide
FT Domain /label= Extracellular_domain
FT Domain 323..353
FT Domain /label= Transmembrane_domain
FT Domain 354..864
FT Protein /label= Cytoplasmic_domain
FT Protein 32..864
FT Protein /label= IL-17R
XX
PN US6072037-A.
XX
PD 06-JUN-2000.
XX
PF 12-FEB-1998; 98US-0022696.
XX
PR 21-MAR-1996; 96US-0620694.
PR 23-MAR-1995; 95US-0410535.
PR 07-AUG-1995; 95US-0538765.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Fanslow WC, Spriggs MK, Yao Z;
XX
DR WPI; 2000-411206/35.
DR N-PSDB; AAA61238.
XX
PT Antibodies immunoreactive with interleukin-17 receptor protein useful
PT in interfering with receptor binding to CTLA-8, as components of
PT diagnostic or research assays or in affinity purification of the
PT receptor -
XX
PS Claim 1; Column 25-30; 25pp; English.
XX
CC The present invention relates to a novel receptor that binds Interleukin
CC 17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog,
CC HVS13. The receptor is a type I transmembrane protein which is referred
CC to as IL-17R. Murine thymoma EL4 cells were found to express a
CC receptor for IL-17. An EL4 mammalian expression library was screened
CC and a cDNA encoding the receptor was identified. The present sequence
CC is the murine IL-17R protein. The cDNA was used to isolate DNA encoding
CC human IL-17R by cross species hybridisation. The human IL-17R cDNA and
CC protein are described in AAA61240 and AAY99941. Soluble forms of the
CC receptor may be used to regulate immune responses, for example to
CC suppress rejection of organ grafts. Antibodies to IL-17R consisting of
CC amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be useful
CC as components of diagnostic or research assays. Such antibodies may also
CC be used in affinity purification of the receptor.
XX
SQ Sequence 864 AA;

Query Match 100.0%; Score 1766; DB 21; Length 864;
Best Local Similarity 100.0%; Pred. No. 8.6e-169; Indels 0; Gaps 0;
Matches 322; Conservative 0; Mismatches 0;

QY 1 MAIRRCWPRVVGPAALGMLLLNLVLAEGRASPRLLDFPAPVCAOEGISCRVKNSTCIDD 60
DB 1 mairrcwprvvgpalgwmlllnvlapgrasprlldfpapvcaeglsrcknstdcid 60
QY 61 SWIHPKMLTSSPKNTYINLSVSTOGELVPLVAVETLQTDASTLYIEGALSLYQIN 120
DB 61 swihpkmltsspknyinlsvstqhgelyplvavetlqtdastllyegalsylvlqin 120
QY 121 TNERLCYKFOFLSMLOHHRKRMRFSESHFVVDPOGEYEVTHLKPDPDGPDNHRSKII 180
DB 121 tnerlcvkfgflsmldghnrkwrtsfshfvvdpggeyevtnhlppdpdgdpnhkskii 180
QY 181 FVPDCEDSKMKMTSCVSSGSLMDPNITVEITLDTQHLRYDFTLNNESPYYQVLLSEFSDS 240
DB 181 fvpdcedskmmtscvssgslwdpnitveltdtqhlrvdftlwnespyqyllsefsds 240
QY 241 ENHSCFVVKOIFAPROEHEFORANVTFTLSKFHMCCHHVOVOPFSSCLMDCIRHAYT 300
DB 241 enhscfdvkvqifaprggefgravtftlskfhwcchhvgvqpfssclndcrlrhayt 300
QY 301 VPCPVISNTTYPKPVADYIPIM 322
DB 301 vpcpvlsnttvpkpvadyipim 322
RESULT 7
AA997130
ID AAY97130 standard; Protein; 864 AA.
XX
AC AAY97130;
XX
DT 04-DEC-2000 (first entry)
XX
DE Murine interleukin-17 receptor.
XX
IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW HVS13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW anti-asthmatic.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Protein 1..322
FT Peptide /label= Soluble_IL-17_receptor
FT Protein 1..31
FT Peptide /label= Signal_peptide
FT Protein 32..864
FT Domain /label= Mature_protein
FT Domain 32..322
FT Domain /label= Extracellular_domain
FT Domain 323..343
FT Domain /label= Transmembrane_domain
FT Domain 344..864
FT Domain /label= Cytoplasmic_tail
XX
PN US6100235-A.
XX
PD 08-AUG-2000.
XX
PF 11-FEB-1998; 98US-0022260.
XX
PR 21-MAR-1996; 96US-0620694.
PR 23-MAR-1995; 95US-0410535.
PR 07-AUG-1995; 95US-0538765.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Fanslow WC, Spriggs MK, Yao Z;
XX
DR WPI; 2000-548298/50.
DR N-PSDB; AAA51987.
XX

Regulating, treating or preventing immune or inflammatory response in a mammal, especially organ or graft rejection, allergy or asthma, comprises administering interleukin-17 receptors

Claim 1: Column 25-30; 26pp; English.

A novel interleukin-17 receptor (IL-17R) was identified by screening a cDNA library from T cell thymoma EL4 cells, which were identified as binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc region and soluble IL-17 (CTLA-8) protein or a homologous Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an immune or inflammatory response in a mammal comprises administering soluble IL-17R. Soluble IL-17R fragments comprise residues 1-322 of the murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the extracellular domain that bind IL-17. The method is useful for regulating an immunoreponse, for treating or preventing diseases like allergy, asthma and autoimmune diseases, and for suppressing rejection of grafted organs or tissues in the recipient.

Sequence 864 AA:

Query Match 100.0%; Score 1766; DB 21; Length 864;
Best Local Similarity 100.0%; Pred. No. 8,6e-169;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAIRRCMPRVVPGPALGMLLLNLVLAAGRASPRLDPAPVCAQEGLSGVKSTCDD 60
DB 1 mairrcmprrvpgpalgwmlllnvlagrasprlldfpavcagqglscrvkstcldd 60
QY 61 SWIHPKRLTPSSPKNTIYNLVSSTQHGELVPVLHVEWTLQTDASIIYLEGAEISVLQ 120
DB 61 swihpknltppspkntiynlsvstqhgelpvvlhvwetlqtdasillylegaelsvqln 120
QY 121 TNERLCVAKROFSLMDLHKKRMKRFSESHFVVDGQEEVYVNHLPKRIPOGDPNKKSKII 180
DB 121 tnerlcvkrfqfslmdlhkkrmkrfseshfvdgqeeyvynhlpkripdgdpnhkskii 180
QY 181 FVPDCEDSKMKMTSCVSSGSLMDPNITVETLDTQHLRVDFTLNNESTPYGVLLSEFS 240
DB 181 fvpdcedskmkmtscvssgslmdpnitvetldtqhrlvdfnlwneestpygvllsefsds 240
QY 241 ENHSCFDVVKQIFAPROEERORANVTFTLSKPFHMCCHHHVOVQPFSSCLNDCLRHNAV 300
DB 241 enhscfdvkvqifaproeerorantvftlskpfhmcchhhvovqpfssclndclrhnavt 300
QY 301 VPCPVISNTTVKRPVADYIPLW 322
DB 301 vpcpvistntvtpkpvadyiplw 322

```

RESULT 8

AA97180
AA97180 standard; Protein; 864 AA.

AA97180;

04-DEC-2000 (first entry)

Murine interleukin-17 receptor.

IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri; HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic; anti-asthmatic.

Mus sp.

Key Location/Qualifiers

Protein 1..322

Peptide 1..31

Protein /label= Signal_peptide 32..864

Domain /label= Mature_protein 32..322
Domain /label= Extracellular_domain 323..343
Domain /label= Transmembrane_domain 344..864
Domain /label= Cytoplasmic_tail

US6096305-A.

01-AUG-2000.

11-FEB-1998; 98US-0022253.

21-MAR-1996; 96US-0620694.

23-MAR-1995; 95US-0410535.

07-AUG-1995; 95US-0538765.

(IMNV) IMMUNEX CORP.

Fanslow WC, Spriggs MK, Yao Z;

WPT: 2000-523862/47.

N-PSDB; AAA52145.

Suppressing rejection of a grafted syngeneic or allogeneic organ or tissue in a graft recipient for organ transplantation involves transfecting the organ or tissue with DNA encoding soluble interleukin-17 receptor

Claim 1: Column 25-30; 27pp; English.

A novel interleukin-17 receptor (IL-17R) was identified by screening a cDNA library from T cell thymoma EL4 cells, which were identified as binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc region and soluble IL-17 (CTLA-8) protein or a homologous Herpesvirus saimiri (HSV) protein, designated HSV13. Suppressing rejection of a grafted syngeneic or allogeneic organ or tissue in a graft recipient involves transfecting the organ or tissue to be transplanted with DNA encoding soluble IL-17R, so that expression of IL-17R by the engrafted organ or tissue results in suppression of rejection. Soluble IL-17R fragments comprise residues 1-322 of the murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the extracellular domain that bind IL-17. The method is useful for regulating an immunoreponse, for suppressing rejection of grafted organs or tissues in the recipient and for treating or preventing diseases like allergy, asthma and autoimmune diseases.

Sequence 864 AA:

Query Match 100.0%; Score 1766; DB 21; Length 864;
Best Local Similarity 100.0%; Pred. No. 8,6e-169;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAIRRCMPRVVPGPALGMLLLNLVLAAGRASPRLDPAPVCAQEGLSGVKSTCDD 60
DB 1 mairrcmprrvpgpalgwmlllnvlagrasprlldfpavcagqglscrvkstcldd 60
QY 61 SWIHPKRLTPSSPKNTIYNLVSSTQHGELVPVLHVEWTLQTDASIIYLEGAEISVLQ 120
DB 61 swihpknltppspkntiynlsvstqhgelpvvlhvwetlqtdasillylegaelsvqln 120
QY 121 TNERLCVAKROFSLMDLHKKRMKRFSESHFVVDGQEEVYVNHLPKRIPOGDPNKKSKII 180
DB 121 tnerlcvkrfqfslmdlhkkrmkrfseshfvdgqeeyvynhlpkripdgdpnhkskii 180
QY 181 FVPDCEDSKMKMTSCVSSGSLMDPNITVETLDTQHLRVDFTLNNESTPYGVLLSEFS 240
DB 181 fvpdcedskmkmtscvssgslmdpnitvetldtqhrlvdfnlwneestpygvllsefsds 240
QY 241 ENHSCFDVVKQIFAPROEERORANVTFTLSKPFHMCCHHHVOVQPFSSCLNDCLRHNAV 300
DB 241 enhscfdvkvqifaproeerorantvftlskpfhmcchhhvovqpfssclndclrhnavt 300

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Db 241 enhscidvkvqilaprggefgrnavfltskfhwccbhvqvpfissclndclrhavt 300

OY 301 VPCPVISNTTVPKRVADYIPLM 322

Db 301 VPCPVISNTTVPKRVADYIPLM 322

Db 301 vpcpvlsnttvpkpvadyiplw 322

RESULT 9

AAB03806

ID AAB03806 standard; Protein: 864 AA.

XX AAB03806;

AC AAB03806;

DT 13-OCT-2000 (first entry)

DE Murine interleukin-17 (IL-17) receptor protein sequence.

XX Interleukin-17 receptor; IL-17R; CTLA8; antiinflammatory; antiallergic;

KW immunosuppressive; organ rejection; graft rejection; autoimmune disease;

KW allergy; asthma; mouse.

OS Mus sp.

XX US6072033-A.

PN 06-JUN-2000.

PD 11-FEB-1998; 98US-0022255.

PF 21-MAR-1996; 96US-0620694.

PR 23-MAR-1995; 95US-0410535.

PR 07-AUG-1995; 95US-0538765.

XX (IMMV) IMMUNEX CORP.

PI Fanslow WC, Spriggs MK, Yao Z;

DR WPI: 2000-411205/35.

DR N-PSDB: AAF59870.

PT Interleukin-17 receptor protein useful for regulating immune functions

PT and for preventing or treating organ or graft rejection, autoimmune

PT disease, allergy or asthma in human

PS Claim 1; Column 25-30; 26pp; English.

XX This invention relates to an isolated and purified interleukin-17

CC receptor (IL-17R). A soluble IL-17 protein (CTLA8) and a herpesvirus

CC siamuri (HVS13) open reading frame (homologous to CTLA8) were expressed

CC as fusion proteins comprising an immunoglobulin Fc region, and used to

CC screen for the expression of the IL-17R. The screening identified the

CC novel receptor of the invention. IL-17R is a type I transmembrane

CC protein that exhibits antiinflammatory, immunosuppressive, antistatic

CC and antiallergic activities, and is an inhibitor of T cell proliferation

CC and activation. IL-17R can be used to regulate immune functions, and is

CC useful for preventing or treating organ or graft rejection, autoimmune

CC disease, allergy or asthma. The present sequence represents the murine

CC interleukin-17 receptor amino acid sequence identified in the invention.

XX Sequence 864 AA:

SQ

Query Match 100.0%; Score 1766; DB 21; Length 864;

Best Local Similarity 100.0%; Pred. No. 8 6e-169;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAIRRCMPRVVPGALGWLILLNLVLAAGRASPRLLDPAPVCAQEGLSCKRVKSTCLDD 60

Db 1 maltrrcwprvvpalqwlillnlvlapgrasprllldfpavcageglsckrvkstcldd 60

OY 61 SMHPRKRLTSSSKRNITINISVSTOGCELVPVLAHEWTLDTASILYLEGAEISVLOLN 120

Db 61 swlhpkrlltsssknlylnisvstgclvlpvlhewtltdasillylegelsvllqin 120

OY 121 TNERLCVKFOFLSLQHRKRWRFESHFVYDPCOEYEVTHHLKPIPDGDPNKRKII 180

Db 121 tnerlcvkfgflsmldqhrkrwrfeshfvvdpcogeyevthhlpkipdgdpnkrskii 180

OY 181 FVPDCEDSKMKMTSCVSSGLMPDNITVETLDQRLRVDFTLNES7PYOVLESFSDS 240

Db 181 fvpdcedskmkmtscvssgslwdpnltvetldtqhlrvdftllwnes7pyvllsfds 240

OY 241 ENHSCPDVVKQIPAPRDEFFHQANVTFTLSKFWCCHHHVOVQPFSSCLNDCIRHAVT 300

Db 241 enhscidvkvqilaprggefgrnavfltskfhwccbhvqvpfissclndclrhavt 300

OY 301 VPCPVISNTTVPKRVADYIPLM 322

Db 301 vpcpvlsnttvpkpvadyiplw 322

RESULT 10

AAB62060

ID AAB62060 standard; Protein: 864 AA.

XX AAB62060;

AC AAB62060;

DT 29-MAY-2001 (first entry)

DE Murine IL-17R polypeptide.

XX CTLA-8; interleukin-17; IL-17; IL-17 receptor; IL-17R; mouse;

KW immunosuppressive; antiallergic; antisthmatic; antiinflammatory.

OS Mus sp.

XX Key location/Qualifiers

FT Peptide 1..31

FT Protein /note= "signal peptide"

FT Domain /note= "32..864"

FT Domain /note= "mature protein"

FT Domain /note= "32..322"

FT Domain /note= "extracellular domain"

FT Domain /note= "323..343"

FT Domain /note= "transmembrane domain"

FT Domain /note= "344..864"

FT Domain /note= "cytoplasmic domain"

PN US6197525-B1.

XX 06-MAR-2001.

PD 11-FEB-1998; 98US-0022257.

PF 21-MAR-1996; 96US-0620694.

PR 23-MAR-1995; 95US-0410535.

PR 07-AUG-1995; 95US-0538765.

XX (IMMV) IMMUNEX CORP.

PI Yao Z, Spriggs MK, Fanslow WC;

DR WPI: 2001-234480/24.

DR N-PSDB: AAF57186.

PT New assay kits for detecting interleukin-17 (IL-17), IL-17 receptors

PT and (antagonists or mimetics of) the interaction between IL-17 and

PT IL-17 receptor, useful for treating autoimmune diseases -

PS Claim 1; Columns 19-26; 26pp; English.

XX The invention is directed towards assays for detection of interleukin-17

CC (IL-17), IL-17 receptor (IL-17R), and (antagonists or mimetics of) the

CC interaction between IL-17 and IL-17R. The assay kit comprises an IL-17R

CC protein and a detecting reagent. The method is useful for inhibiting

CC binding of IL-17 to cells expressing IL-17R. IL-17 receptors are also

CC useful for preventing or treating organ or graft rejection, autoimmune
CC diseases, allergy, asthma and inflammatory diseases in which activated
CC T-cells play an important role. The present sequence represents a
CC mouse IL-17R polypeptide.

5Q Sequence 864 AA;

Query Match	100.0%	Score 1766:	DB 22:	Length 864:
Best Local Similarity	100.0%	Pred. No. 8.6e-16:		
Matches 322:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0

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Db	1	MAIRTCRPVYVVPBAPLWLIILNVLAPGASPRILDFRPRVCAOAGELSCRUVNSICLD	60
QY	61	SWIHPKNLPRSSPKNIYINLVSSTOHEGLVPLVHVEWTLQTDASILYEGAEISVLDQIN	120
Db	61	SWIHPKLIPTSPSPNIYINLVSSTQHEGLVPLVHVEWTLQTDASILYEGAEISVLDQIN	120
QY	121	TNEHLCKPQFLSLMDHNRKRWPRSFHFVAVDGGQEEVYVNHLPKPIPCGDRNHKSKII	180
Db	121	TNEHLCKPQFLSLMDHNRKRWPRSFHFVAVDGGQEEVYVNHLPKPIPCGDRNHKSKII	180
QY	181	FVPDCEDSKKMMFTTSCVSSGSLMDPNITVEETLDTQHLRVDFLTLMNESTPYQVLLSEPSDS	240
Db	181	FVPDCEDSKKMMFTTSCVSSGSLMDPNITVEETLDTQHLRVDFLTLMNESTPYQVLLSEPSDS	240
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Db	241	ENHSCGFVYVQIFAPRQEEFHORANVYFTLSKRWCCNHNVQVOPFSSCLNOCILHAYT	300
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Db	301	VPCPVSINNTVPKPVADYITLW 322	

RESULT	11
AAV72748	
ID	AAV72748 standard; Protein; 864 AA.

AC	AAY72748;
XX	
DT	31-MAY-2001 (first entry)

Murine Interleukin-17 receptor (IL-17R) or CTLA-8 receptor.

KM Murine interleukin-17 receptor; IL-17R: immunosuppressive; antiallergic;
 KM inflammatory disease; allergy; Ccr4-8; immunogen; asthma.
 KM inflammatory disease; allergy; Ccr4-8; immunogen; asthma.

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FT      /label= Signal_peptide
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FT /label= Mature_murine_IL-17_receptor
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FT	label= Extracellular_domain
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/label= Transmembrane_domain

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/label= Cytoplasmic_tail

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PN US6191104-B1.

PD 20-FEB-2001.

PF 11-FEB-1998; 98US-0022259.

PR 21-MAR-1996; 96US-0620694.

PR 07-AUG-1995; 95US-0538765.

PA (IMMV) IMMUNEX CORP.

PI Spriggs MK, Fanslow WC;

DR WPI; 2001-217901/22.

XX

PT involves administering to recipient a composition comprising

XX

XX

CC CTLA-8 receptor.

Interleukin-17 and their corresponding nucleic acid molecules. IL-17R is an invariant, shared receptor for IL-17. IL-17 is a type I transmembrane protein which is used for regulating the immune response. The invention is useful for suppressing rejection of a grafted organ or tissue in a graft recipient. Soluble IL-17 (CpA-8) receptors are useful for preventing or treating organ or graft rejection, autoimmune disease, allergy, asthma, and inflammatory disease in which activated T-cells play a role. Soluble IL-17 fusion proteins are used to screen cells for the expression of IL-17 receptor. Derivatives of IL-17R are also used as immunogens, reagents in *in vitro* assays, or as binding agents for affinity purification procedures.

SQ Sequence 864 AA;

Query Match	100.0%	Score 1766;	DB 23;	length 864;
Best Local Similarity	100.0%	Pred. No. 8.6e-169;		
Matches 322;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MAIRCRWRYVPGALIGWLLLLLVWAPGRASPRLLDPRAVNAOEGISCVKSTCIDD	60
Db	1	mairrcwrvvpgaligwlllllvlapgrasprlldrprvcsaqegiscvknstctidd	60
Qy	61	SMIHRKNTPSSPKNIYVNLSSVSTQHELVPLHVEVTLQTDASIIYLEGAEISVQLN	120
Db	61	swihpknltprspkriynlnlssvstqhgelyvplhveweklqtcdsilylegaelsvqqln	120
Qy	121	TNERLCVCFQCLSMLOHRRKRMRESFSHFVVDPCQOEVEVYVNHDKRIPDDGPNHKSII	180
Db	121	tnerlcvcfqfqlsmloghrrkrmrwsfsstfvvdprqgeyevvnhlprkprpdgdpnhkskii	180
Qy	181	FVPDCEDSKMKMTTSCVSSGSLMDPNITVETLDTQHLRVDFTLNNESTPIYVULLESFSDS	240
Db	181	fvpdcedsckmkmttscvssgslwdpnlvletldtqhlrvdftlwnestpiyvllesfss	240
Qy	241	ENHSCFEDVVKOIFAPROGEFHORANVTTLTSKFWMCCHNNHQVQRFSSCLNDCLRNAVY	300
Db	241	enhscfdvkvqifaprggefhqranvvtltskfmcchhqvqpfissclndclrhnavt	300
Qy	301	VPCPVISNTVPRVADYIPLM 322	
Db	301	vpcpvistntlvprvadylptlw 322	

RESULT	12
AAW04185	
ID	AAW04185 standard; Protein; 866 AA

AC AAW04185;

DT 05-DEC-1996 (first entry)

DE Human interleukin-17 receptor.

KW Interleukin-17 receptor; IL-17R; autoimmune disease; allergy;

Job time: 193 sec

PN US6072037-A.
XX
PD 06-JUN-2000.
XX
PF 12-FEB-1998; 98US-0022696.
XX
PR 21-MAR-1996; 96US-0620694.
PR 23-MAR-1995; 95US-0410535.
PR 07-AUG-1995; 95US-0538765.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Fanslow WC, Spriggs MK, Yao Z;
XX
DR WPI; 2000-411206/35.
XX
N-PSDB; AAA61240.

PT Antibodies immunoreactive with interleukin-17 receptor protein useful
PT in interfering with receptor binding to CTLA-8, as components of
PT diagnostic or research assays or in affinity purification of the
PT receptor -

PS Claim 1; Column 43-48; 25pp; English.

XX
XX
CC The present invention relates to a novel receptor that binds Interleukin
CC 17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog,
CC HVS13. The receptor is a type I transmembrane protein which is referred
CC to as IL-17R. Murine thymoma EL4 cells were found to express a
CC receptor for IL-17. An EL4 mammalian expression library was screened
CC and a cDNA encoding the receptor was identified. The murine IL-17R cDNA
CC and protein are described in AAA61238 and AAY99935. The cDNA was used to
CC isolate DNA encoding human IL-17R by cross species hybridisation. The
CC present sequence is the human IL-17R protein. Soluble forms of the
CC receptor may be used to regulate immune responses, for example to
CC suppress rejection of organ grafts. Antibodies to IL-17R consisting of
CC amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be
CC useful as components of diagnostic or research assays. Such antibodies
CC may also be used in affinity purification of the receptor.

SO Sequence 866 AA;

Query Match 71.08; Score 1254; DB 21; Length 866;
Best Local Similarity 71.48; Pred. No. 2.8e-117;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

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DB 1 mgarssppsavpgjllglllllgvlapggsalrllldhralvcspglnctvknstcldd 60
QY 61 SWIHPKMLTSPSPKNITYINLSVSSSTOGEELVPLHVEWTLOTDASTLYEGAEISVLOLN 120
DB 61 swihprnltpsspsdldqqlfahntqgdflfvahlewlitqdasllylegaelsvlqln 120
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DB 301 vscpempdt-pepdpdympiw 320

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